

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 197922

**TO: Ginny Portner** 

Location: REM/3B02/3C18

**Art Unit: 1645** 

Monday, August 14, 2006

Case Serial Number: 10/764212

From: Vira David

**Location: Biotech-Chem Library** 

**REM-1A41** 

Phone: (571)272-1972

Virajita.David@uspto.gov

#### **Search Notes**

Examiner Portner,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Vira David Intern STIC Biotech/Chem Library (571)272-1972





## STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

Vol	untary Results Feedback Form						
>	I am an examiner in Workgroup: Example: 1610						
×	Relevant prior art found, search results used as follows:						
	☐ 102 rejection						
	☐ 103 rejection						
	☐ Cited as being of interest.						
	Helped examiner better understand the invention.						
	Helped examiner better understand the state of the art in their technology.						
•	Types of relevant prior art found:						
	☐ Foreign Patent(s)						
	<ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul>						
>							
	Results verified the lack of relevant prior art (helped determine patentability).						
	Results were not useful in determining patentability or understanding the invention.						
Co	mments:						

Drop offor send completed forms to STIC/Biotech-Chem Library: Remsen Bidgs



#### STIC-Biotech/ChemLib

197922

From: Portner, Ginny

Sent: Tuesday, August 08, 2006 12:54 PM

To: STIC-Biotech/ChemLib

**Subject:** 10/764,212

please search sequences 16, 18 and 20, and oligomer search with respect to amino acid sequences

Ginny Portner Remsen Building Art Unit 1645 Room E03, B02; Mail Box 3C18 (571) 272-0862

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Result
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Maximum Match 100%
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·	Aeb70205 H. pylori Aeb70211 Helicobac Aeb70154 H. pylori Aeb70212 Helicobac Abu51720 Helicobac	H H H H	Adj27351 Alpha-1,3 Aeb70137 Helicobac Aeb70204 H. pylori Aeb70203 H. pylori Aeb70203 H. pylori	Aeb70195 H. pylori Aeb70149 Helicobac Aeb70197 H. pylori Adj77816 Helicobac

# ALIGNMENTS

Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO:

16.

06-OCT-2005 AEB70145;

(first entry)

AEB70145 standard; protein;

446

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WPI; 2005-521417/53.
N-PSDB; AEB70144.
                                                                                                                                                                                                                                         Location/Qualifiers Misc-difference 168
                Claim 1; SEQ
                              New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                Simala-Grant J,
                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                              Misc-difference 408
                                                                                                                                                                                                                               Misc-difference
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                                                                                               (NEOS-) NEOSE TECHNOLOGIES INC. (UYAL-) UNIV ALBERTA.
                                                                                                                       22-JAN-2004; 2004US-00764212.
                                                                                                                                      22-JAN-2004; 2004US-00764212.
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                                                                                                                                                                                                                                                                     Helicobacter pylori; strain 1111.
                ID NO 16;
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                                                                               Taylor D,
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                97pp; English.
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The present invention provides alpha-1,3/4-fucosyltransferase (also

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29-MAR-1999
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    Peptide
                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                     AAW86008 standard; protein;
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fucosyltransferase of Helicobacter pylorin NCTC 1639, as deduced from the
newly isolated fucT gene (see AAV80321). The enzyme is characterised by 8
C-terminal heptad repeats and by the lack of a transmembrane domain. The
absence of a transmembrane domain allows the enzyme to be readily
released from recombinant host cells. The enzyme can be used in the
production of fucosylated oligosaccharides such as Lewis X, Lewis Y and
sialyl Lewis X, which are structurally similar to certain tumour
associated antigens found in mammals. These glycoconjugates also have
research and diagnosis utility in the development of assays to detect
mammalian tumours. The enzyme can also be used to raise specific
antibodies. Inhibition of abnormal fucT gene product activity can be used
for the treatment of intestinal mucosal disease. (Updated on 17-OCT-2003
to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated alpha-1-3-fucosyltransferase gene - obtained from Helicobacter pylori, used to develop products for the diagnosis treatment of intestinal mucosal diseases, e.g. tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059913/05.
N-PSDB; AAV80321.
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                                                                                                                                                                        Similarity
                                                                                                                      MPQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEBIKEFKKSVLYFIFSQRYTIALH
              RMPLYYDRLHHKAESVNDTTS PYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR
                                                                    QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL 120
 RMPLYYDRLHHKAESVNDTTAPYKLKDNSLYALKKPSHCFKEKHPNLCAVVNDESDPLKR
                                                   QNPNEFSDLVFGNPLGSARKILSYQNAKRVFYTGENESPNFNLFDYAIGFDELDFNDRYL
                                                                                                       MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKNSVLYFILSQRYTITLH
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                                                                                                                                                           Conservative
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/note=
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378. .384
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;35. .437
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.412
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.398
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.405
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87.1%;
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.377
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                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is N-glycosylated"
                                                                                                                                                           Score 2081; DB 2;
Pred. No. 3.9e-174;
Fig. Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat"
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                                                                                                                                                            16;
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GVVSFVASNANAPMRNAFYDALNS I E PVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN

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                  Purified transmembrane segment-free alpha1,3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                             N-PSDB;
                                                                                                              05-JUN-1998;
                                                                                                                               07-DEC-2000; 2000US-00733524.
Claim 6; Fig 2A; 37pp;
                                                                         Taylor DE,
                                                                                                                                                                    US2002068347-A1.
                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                  Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley; sLex; Helicobacter pylori infection; malignant cell; mammalian tumour
                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori alphal, 3 fucosyltransferase #1.
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                                                                                           (UYAL-) UNIV ALBERTA.
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                                             2002-582480/62.
DB; ABK89249.
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272
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                                                                                                                                                                                                                                                                               /note= "Encoded by CTG" 264
                                                                                                                                                                                                                                                                                                   214
                                                                                                                                                                                                                          /note= "Bncoded 278
                                                                                                                                                                                                                                                             /note= "Encoded by TGG" 269
                                                                                                                                                                                     /note= "Encoded by GT"
465. .501
/note= "Region not encoded by sequence appearing
ABK89249"
                                                                                                                                                                                                                                                                                                         note= "Encoded by ACTC"
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English
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Critically contacting the produced oilgosaccharides, or purifying the botained oilgosaccharides. The mucleic acid is useful contacting the botained oilgosaccharides. The mucleic acid is sufficient or producing the protein contacting the protein complement or fragment), a vector containing the nucleic complement or fragment), a vector containing the nucleic contacting the protein acid and a gene expression system for compressing a host cell containing nucleic acid or vector, an antibody which complement or fragment), a vector containing the nucleic compressing a host cell modified with the nucleic acid or its compressing a host cell modified with the nucleic acid or stex. By contacting the protein with a substrate such as Lax, Ley or slex, by contacting the protein with a substrate, to produce oilgosaccharides, and colls are useful for contacting the host cell with a substrate, to produce oilgosaccharides and purifying the obtained oilgosaccharides. The nucleic acid is useful contacting the coll with a substrate, to produce oilgosaccharides contacting a sample with a conjunction and detecting the nucleic acid, by contacting a sample with a conjunction and detecting hybridises to alphal, 3-fucosyltransferase conjunction protein protein protein, by growing the host cell is useful for producing a transmembrane segment-free alphal, 3-fucosyltransferase gene product acid using polymerase colling a desired polypeptide corporably linked to a polynucleotide encoding a desired polypeptide corporably linked to a polynucleotide encoding a desired polypeptide corporably linked to a polynucleotide encoding a desired polypeptide corporably linked to a polynucleotide encoding a desired polypeptide corporably in the protein in a sample. The presence of the protein in the protei
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Sequence 501 AA;

Query Match

86.8%; Score 2073; DB 5; Length 501;

Best Local Similarity 87.1%; Pred. No. 2.2e-173;

Matches 393; Conservative 15; Mismatches 27; Indels 16; Gaps

먉 S 밁 8 δ 밁 밁 S 맑 ঠ 밁 S 뭐 ঠ 407 241 181 121 61 61 PLASIDDLRV--------NYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVN 406 SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTH RMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQPKENHPNLCAVVNDESDPLKR 180 MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH 60 YERLLONASPLIBLSONTSFKIYRKAYOKPI 437 KNAYLDMLYENPLNTLDGKAYFYQNLSFKKILAFFKTILENDTIYH--DNPFIFCRDLNE PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLDE TOGYGYVTEKIIDAYFSHTIPIYQGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLHTH RMPLYYDRLHHKAESVNDTTAPYKLKDNSLYALKKPSHCFKEKHPNLCAVVNDESDPLKR YERLLSKATPLLELSONTTSKIYRKAYOKSL 449 PLYTIDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRVN 360 300 240 240 180 358 60

ABG30887 standard; protein; 454

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                                                                                                                                                                                                                                                                                                                             The invention relates a purified transmembrane segment-free alpha 1,3-CC fucushry-K3-X4-Tyr, where X1, X2 and X4 is Asp or Asn; and X3 is CC lle, Val or Als. Also included are the nucleic acid encoding the protein CC acid, a host cell containing nucleic acid or vector, an antibody which CC selectively binds to the protein and a gene expression system for CC producing transmembrane segment-free alphal, 3- fucosyltransferase, CC comprising a host cell modified which encoding the protein for CC producing transmembrane segment-free alphal, 3- fucosyltransferase, CC comprising a host cell modified with a mucleic acid or its contacting the protein with a substrate such as Lex, Ley or slex, by CC contacting the protein with a substrate such as LacNac-R and GDP-fucose, CC and purifying the produced oligosaccharides, such as Lex, Ley or slex, by CC contacting the host cell with a substrate, to produce oligosaccharides are useful for produced oligosaccharides. The nucleic acid is useful cas a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridises to alphal, 3-fucosyltransferase CC amplifying the nucleic acid using polymerase chain reaction (PCR). The host cell is useful for producing a transmembrane segment-free alphal, 3-fucosyltransferase-fusion protein, by growing the host cell containing a created protein and isolating the fusion protein. Browing the host cell containing a cc vector operably linked to a polynucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein in the sample with a substrate protein in the sample is indicative of infection by Helicobacter pylori or the presence of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alphal, 3- and contained the produced acid is useful as gart of ribozyme and/or triple helix sequences and for alphal, 3- and contained the produced acid is useful as a protein and contained acid is u
                                                             fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alphal, 3 fucosyltransferase encdoed by the fucT gene. (Updated on 29-AUG-2003 to standardise OS field)
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21-OCT-2002
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(first entry)
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  Query Match
Best Local Similarity
Matches 383; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 454
                                                                                                                                                                                                                                                                                                         H. pylori alpha1,3 fucosyltransferase #4.
                                                                                                                                                                                                                                                                                                                                                                                                ABG30884 standard;
                                                                                                                                                                                                                                                                    Enzyme; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex;
sLex; Helicobacter pylori infection; malignant cell; mammalian tu
                                                                                                                                                                                                                                                                                                                                  29-AUG-2003
21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                        ABG30884;
                       purified transmembrane segment-free alphal,3-fucosyltransferase
polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                         05-JUN-1998;
                                                                                                                                                                07-DEC-2000; 2000US-00733524.
                                                                                                                                                                                            06-JUN-2002
                                                                                                                                                                                                                    US2002068347-A1
                                                                                                                                                                                                                                           Helicobacter pylori; strain 26695A.
Example 3; Fig 6; 37pp; English.
                                                                WPI; 2002-582480/62.
                                                                                        Taylor DE,
                                                                                                               (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNPDKPADIVFGNPLGSARKILSYQNTKRIFYTGENESPNFNLFDYAIGFDELDFRDRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNPNEFSDLVFSNFLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASPLLELSONTSFKIYRKIYOKSL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASI-----DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKBFVNVHDENNFDEAIDYIKYLHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVVSFVASNANAPMRNAFYDALNSIBPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASPLLELSONTSFKIYRKAYOKPI 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVSIDNLRINYDNLRVNYDDLRVNYDDLRVNYDDLRINYDDLRINYDDLRINYBRLLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNAYLDMLYENPLNTLDGKAYFYQNLSFKKILDFFKTILENDTIYH--NHPFIFYRDLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYVRYLHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMPLYYDRLIHKAESVNDTTAPYKIKGNSLYTLKKPSHCFKENHPNLCALINNESDPLKR
                                                                                        Ge Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                          98US-00092315.
                                                                                                                                                                                                                                                                                                                                                                                                protein; 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.5%; Score 2064.5;
86.3%; Pred. No. 1.16
tive 27; Mismatches
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(including the complement or fragment), a vector containing the nucleic caid, a host cell containing nucleic acid or vector, an antibody which comparising thanks to the protein and a gene expression system for comprising thanks to the protein and a gene expression system for comprising a host cell modified with the nucleic acid or its enzymatically active portion. The protein and cells are useful for producing fucosylated oligosaccharides, such as Lex, Ley or sLex, by contacting the protein with a substrate such as LackNac-R and GDP-fucose, and purifying the produced oligosaccharides, or by culturing the cell with a substrate, to produce oligosaccharides and purifying the obtained oligosaccharides. The nucleic acid is useful as a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridises to alphal, 3-fucosyltransferase complifying the nucleic acid with a substrate segment-free alphal, 3-fucosyltransferase complifying the nucleic acid using polymerase chain reaction (PCR). The host cell is useful for producing a transmembrane segment-free alphal, 3-fucosyltransferase fusion protein, by growing the host cell containing a vector operably linked to a polymucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein and isolative of infection by Helicobacter pylori or the prosence of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alphal, 3-fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple helix sequences and for alphal, 3-gart of ribozyme and/or triple helix sequences and for alphal, 3-gart of ribozyme and/or triple helix sequences and for alphal, 3-gart of ribozyme and/or triple helix sequences and for alphal, 3-gart of ribozyme and/or triple helix sequences and for alphal, 3-gart of call as each and for alphal, 3-gart of call as a sequence and call as useful contained as a sequen The invention relates a purified transmembrane segment-free alpha 1,3-fucosyltransferase polypeptide, having a repeat of the sequence: X\_1-X\_2-fucu-Arg-X\_3-X\_4-Tyr, where X\_1, X\_2 and X\_4 is Asp or Asn; and X\_3 is Leu-Arg-X\_3-X\_4-Tyr, where X\_1, X\_2 and X\_4 is Asp or Asn; and X\_3 is Ile, Val or Ala. Also included are the nucleic acid encoding the protein

Sequence 476

DB 5;

Length 476;

В 8 밁 Ś 밁 Ś 밁 Ś 밁 S 밁 S 밁 Matches 301 300 181 180 121 120 61 394; 60 Similarity HONPNESSDLVFSNPLGAARKILSYONTKRVFYTGENESPNFNLFDYAIGFDELDFNDRY 120 MFQPLLDAYVESASIEKMASKS-PPPLKIAVANWWGDEBIKEFKKSVLYFIFSQRYTIAL HPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLD NSQGYGYVTEKI LDAYFSHTI PI YWGSPSVAKDFNPKEFVNVHDFNNFDEAI DY I KYLHT HPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH--NNPFIFYRDLH NSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYLHT RGFAS FVASNANA PMRNA FYDALNS I EPVTGGGS VRNTLGYKVGNKSEFLSQYKFNLCFE RGVVSFVASNANA PMRNAFYDALNS I EPVTGGGSVKNTLGYNVKNKS EFLSQYKFNLCFE LRMPLYYAHLHYEAELVNDTTAPYKLKDNSLYALKKPSHHFKENHPNLCAVVNDESDLLK LRMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLK HQNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRY MFQPLLDAFIESASIEKMVSKSPPPPLKIAVANWWGDEEIKEFKKSVLYFILSQRYAITL Conservative 86.2%; Score 2058.5; 84.5%; Pred. No. 3.9e 13; Mismatches -----DDLRVNYDDLRVNYDDLRVNYDDLRV 3.9e-172; Indels 31; Gaps 391 180 359 300 240 60

392

NYDDLRVNYDDLRVNYERLLQNASPLLELSQNTSFKIYRKAYQKPI 437

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419 NYDDLRVNYDDLRVNYDRLLQNASPLLELSQNTTFKIYRKAYQKSL 464
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H. pylori alphal, 3 fucosyltransferase
                                                                                                          ABG30886 standard; protein; 479 AA
                                29-AUG-2003
21-OCT-2002
                                                                             ABG30886;
                                (revised)
(first en
                                entry)
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Enzyme; fucT; aipnai, a ruce; slex; Helicobacter pylori infection; fucT; alpha1,3 fucosyltransferase; oligosaccharide; Lex; Ley;
elicobacter pylori infection; malignant cell; mammalian tumour.

Helicobacter pylori; strain 763

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07-DEC-2000; 2000US-00733524.
                                                                                                            06-JUN-2002.
                                                                                                                                              US2002068347-A1.
(UYAL-) UNIV ALBERTA.
                                    98US-00092315.
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Purified transmembrane segment-free alpha1,3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.

WPI; 2002-582480/62.

Taylor DE,

Ge Z;

Example 3; Fig 6; 37pp; English.

RESULT 6
ABG30886
ID ABG3086
ID ABG30886
ID ABG3086
ID ABG308
ID ABG3086
ID ABG3086
ID ABG3086
ID ABG308 CC fucosyltransferase polypeptide, having a repeat of the sequenc: X 1-X 2 (C ILE, Val or Ala. Also included are the mucleic acid encoding the protein CC (including its complement or fragment), a vector containing the protein CC (acid, a host cell containing nucleic acid or vector, an antibody which CC selectively binds to the protein and a gene expression system for CC comprising a host cell modified with the nucleic acid or its complement or fragment), a vector containing the mucleic comprising a host cell modified with the nucleic acid or its comprising a host cell modified with the nucleic acid or its comprising a host cell modified with the nucleic acid or its contacting the protein with a substrate such as Lex, Ley or sLex, by CC contacting the protein with a substrate such as Lex, Ley or slex, by CC contacting the bobtained oligosaccharides, or by culturing the cell, contacting the obtained oligosaccharides, or by culturing the cell, contacting the nucleic acid with a substrate, to produce oligosaccharides contacting a sample with a probe for detecting the nucleic acid, by contacting a sample with a contact cell is useful for producing a transmembrane segment-free alphal, 3-fucosyltransferase fusion protein and isolating bybridisation of the probe; or by amplifying the nucleic acid using polymerase chain reaction (PCR). The consyltransferase fusion protein, by growing the host cell containing a corporately linked to a polymucleotide encoding a desired polypeptide corporately linked to a polymucleotide encoding a desired polypeptide corporately linked to a polymucleotide encoding a desired polypeptide corporately linked to a polymucleotide encoding a desired polypeptide corporate and isolating the fusion protein. The antibody is useful as useful as useful as useful as useful as the protein and isolating the fusion protein and secretion of the protein in the complement of sassays to detect communalian tumours. The present sequence and for alphal, 3-fucosyltransferase gene regulation. Oligosaccharides synth The invention relates a purified transmembrane segment-free alpha 1,3-

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ADJTIT 7
ADJTIT ADJTI
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Matches 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ77814 standard; protein;
        New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is
                                                                                                                                                                            Johnson
                                                                                                                                                                                                                                                                                  23-JUL-2002;
08-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                 23-JUL-2003; 2003WO-US023057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori strain 1218 FutB protein SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ77814;
                                                                                                                                                                                                                                  (NEOS-)
                                                                                                                 2004-123401/12
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                                                                                                                                                                                                                               NEOSE TECHNOLOGIES INC
                                                                                             ADJ77813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGFASFVASNPNAPIRNAFYDALNSIEPVTGGGSVRNTLGYNVKNKNEFTSQYKFNLCFE
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83.7%; Pred. No. 2e-1
tive 15; Mismatches
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Best Local Similarity 81.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycopyroteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 1218 FutB protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; SEQ ID NO 6; 72pp; English.
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-----DLRVNYDDLRVNYERLLQNASPLLELSQNTSFKIYRKAYQKFI 437
                                                                                PNAYLDMLYENPLNTLDGKAYFYQNLSFKKILDFFKTILENDTIYH--DNPFIFYRDLNE
                                                                                                                                                 PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWBCDLDE
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                                                                 PLISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVN
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RESULT 8
ADJ27349
ID ADJ27349 standard; protein; 485 AA.

XX
AC ADJ27349;
XX

DT 20-MAY-2004 (first entry)

XX
DE Alpha-1,3/4-fucosyltransferase.

XX
alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;

XX
Fucosyl; fucose.

XX
Helicobacter pylori; strain 1218 FutB.

XX
WO2004009793-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for the fucose fucosity fucosity substrate to the fucose fucose fucose fucos substrate to the fucose fucose fucos substrate to the fucose fucose fucose fucos substrate to the fucose fucose fucose fucose fucose fucose fucos fucose fuco
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08-NOV-2002; 2002US-0424894P.
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81.6%; Pre/
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RESULT 9 AEB70135 ID AEB7

AEB70135

standard; protein; 485

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Best Local S
Matches 385
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The prese sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 6; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated fucosyltransferase polynucleotides and polypeptides, for synthesizing oligosaccharides, glycoproteins, or glycolipids.
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          361
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DB; AEB70134.
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                                                                                                                                                                                                                                                                                    MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH
                                                                                                                                                                                                                                                                                                                                                                                        485
PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNY----
                                                                                                  SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTH
                                                                                                                                                GVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
                                                                                                                                                                                               RMPLYYDRLHHKAESVNDTTS PYKLKDNSLYTLKKPSHQPKENHPNLCAVVNDESDPLKR
                                                                                                                                                                                                                                                QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL
                                                 PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLDE
                                                                                  SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLHTH
                                                                                                                                   GFAS FVASNPNA PKRNA FYDALNS I EPVIGGGS VKNTLGYNI KNKSEFLSQYKFNLCFEN
                                                                                                                                                                                     RMPLYYDRLHHKAESVNDTTSPYKLKPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKR
                                                                                                                                                                                                                                      QNPNEPSDLVFGSPIGSARKILSYQNAKRVFYTGENESPNFNLFDYAIGFDELDFRDRYL
                                  PNAYLDMLYENPLINTLDGKAYFYONLSFKKILDFFKTILENDTIYH--DNPFIFYRDLNE
                                                                                                                                                                                                                                                                                                                                     85.4%; ilarity 81.6%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                     ; Score 2040.5; DB 9; Pred. No. 1.5e-170; 23; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>\</del>
                                                                                                                                                                                                                                                                                                                                                               9;
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                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                       37;
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RESULT 10
RADJ77810
ID ADJ77810
AC ADJ77
AC ADJ7
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Tr. 18
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides thereof, which are related to the fucosyltransferase enzymes (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycopyroteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 1182 FutB protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori strain 1182 FutB protein SeqID
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08-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2003; 2003WO-US023057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel isolated polynucleotides and the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; SEQ ID NO 2; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
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DB; ADJ77809.
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                                    RMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR
                                                                                            QNPNEPSDLVFGSPIGSARKILSYQNAKRVFYTGENESPNFNLFDYAIGFDELDFRDRYL
                                                                                                                              QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL
                                                                                                                                                                                                              MFQPLLDAYIESASIEKITSKSPPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLH
                                                                                                                                                                                                                                             MPQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH
                                                                                                                                                                                                                                                                                                                                   Conservative
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2002US-0424894P.
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                                                                                                                                                                                                                                                                                                                                                               85.3%; Score 2036;
81.2%; Pred. No. 3.
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3.8e-170;
      Length 486;
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RESULT 11
ADJ27345
ID ADJ27
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                        This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori; strain 1182 FutB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-1,3/4-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ27345 standard;
                                                                                                                                                                                                     Producing fucosylated glycoprotein, by of fucosyltransferase protein with mixture acceptor substrate on glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-1;
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                                                                                                                                                                                                                                                                                                         Johnson
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08-NOV-2002; 2002US-0424894P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fucosyl;
Sequence
                                                                                                                                                                         Claim 1; Fig 1; 84pp; English.
                                                                                                                                                                                                                                                                                                                                    (NEOS-) NEOSE TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLHTH
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   486
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Query Match

85.3%;

Score 2036;

DB 8;

Length 486

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RESULT 12
AEB70131
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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various
                                                       New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                Simala-Grant J,
                                                                                                                                                                                                                                                                US2005164338-A1
                                                                                                                                                                                                                                                                                        Helicobacter
                                                                                                                                                                                                                                                                                                              Fucosyltransferase;
                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID
                                                                                                                                                                                           22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                                                 22-JAN-2004; 2004US-00764212.
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                                                                                                           2005-521417/53.
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|NYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNTTFKIYRKAYQKSL 471
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81.2%; Pred. No. 3.8e-170;
tive 23; Mismatches 28;
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H. pylori alpha1,3 fucosyltransferase 29-AUG-2003 21-OCT-2002 (revised) (first entry)

Helicobacter pylori infection; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley; elicobacter pylori infection; malignant cell; mammalian tumour.

#2.

Helicobacter pylori; strain

US2002068347-A1

06-JUN-2002

07-DEC-2000; 2000US-00733524

05-JUN-1998; 98US-00092315

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Taylor DE, မှ Ņ

WPI; 2002-582480/62

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Ce enzymatically active portion. The protein and cells are useful for contacting fucosylated oligosaccharides, such as Lex, Ley or slex, by cell contacting the protein with a substrate such as LacNAc-R and GDP-fucose, cell and purifying the produced oligosaccharides, or by culturing the cell, contacting the host cell with a substrate, to produce oligosaccharides and purifying the produced oligosaccharides. The nucleic acid is useful cell, as a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridises to alphal,3-fucosyltransferase constructing a sample with a cell is useful for producing a transmembrane segment-free alphal,3-fucosyltransferase-fusion protein, by growing the host cell containing a vector operably linked to a polynucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein and isolating the fusion protein. The antibody is useful for danguosing disorders and monitoring disease, and for inhibiting abnormal alphal,3-cells in the protein or cells. The antibody is also useful for diagnosing disorders fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple halix sequences and for alphal,3-cells fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The presents encoded by the fucT gene. (Updated on 29-AUG-2003 to standardise of field)
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81.2%; Pred. No. 2.9e-169;
tive 23; Mismatches 28; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (PutA and PutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 26695 FutA protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polymucleotide encoding fucosyltransferase protein, us for synthesizing oligosaccharide moiety on a protein or lipid that unglycosylated in its native form or for synthesizing glycolipids.
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08-NOV-2002; 2002US-0424894P.
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fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; SEQ ID NO 12; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                Sequence 425
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                                                                                                                                                                                                                                                     Similarity
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HQNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRY 119
                                                                                                                            MFQPLLDAYVESASIEKMASKS-PPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIAL 59
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Pred. No. 1.2e-164;
9; Mismatches 24;
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                   This sequence represents an alpha-1,3/4-fucosyltransferase protein whicl was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                   Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate acceptor substrate on glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
fucosyl; fucose.
                                                                                                                                                                                                                                                                                                 Example 1; Fig 6; 84pp; English.
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08-NOV-2002;
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DB; ADJ27354.
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LSQNTTFKIYRKAYQKSL
                                           KPLVSIDDLRVNYDDLRVNYD--
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Search completed: August 11, 2006, 19:36:48
Job time: 118.648 secs

Copyright

GenCore version (c) 1993 - 2006

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fucosyltransferase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: C64601
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64601
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A;Cross-references: UNIPROT:025366; UNIPARC:UPI0000D70CB; GB:AE000578; GB:AE000511; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 394;
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NYDDLRVNYDDLRVNYERLLQNASPLLELSQNTSFKIYRKAYQKPI 437
                                                                                         HPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLD 359
                                                                                                                                                     NSQGYGYVTEKILDAYFSHTIPIYMGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHT
                                                                                                                                                                                                                                  RGVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFE 239
                                                                                                                                                                                                                                                                                               LRMPLYYDRLHHKABSVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLK 179
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                                 EPLISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRV
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18; Pred. No. 8.5e-130;

13; Mismatches 28; Indels
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S725284
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A45597
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not

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alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
(;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: B71914
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; 1
Nature 397, 176-180, 1999
Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; pMID:9252185

A;Accession: C64567
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A;Cross-references: UNIPROT:025142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511;
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C;Species: Helicobacter pylori
C;Bate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: C64567
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A; Reference number: A71800; A; Accession: B71914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | LRMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HQNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRY 119
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                                                                                                                                                                                                                                                                                     LSQNTTFKIYRKAYQKSL
                                                                                                                                                                                                                                                                                                                        LSQNTSFKIYRKAYQKPI 437
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                   MUID:99120557;
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Pred. No. 3.9e-:
9; Mismatches
                     PMID: 9923682
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                                                                          E.D.; Doig, P.C.; Smith,
Q.; Taylor, D.E.; Vovis,
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <ARN>
A;Cross-references: UNIPROT:Q9ZLI3; UNIPARC:UPI00000D3665; GB:AE001491; GB:AE001439; NID:
A;Experimental source: strain J99
C;Genetics:
A;Gene: fucT
                                                                                                                                                                                                                                                                                        alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
(;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71862
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, Jives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, Nature 397, 176-180, 1999
                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-436 <ARN>
A;Cross-references: UNIPROT:09ZKD7; UNIPARC:UPI00000D36D2; GB:AE001528; GB:AE001439;
A;Experimental source: strain J99
                                                                                                                                                                                                                                   A; Title: Genomic sequence comparison of two unrelated isolates A; Reference number: A71800; MUID:99120557; PMID:9923682 A; Accession: G71862
                                                                    Query Match
Best Local S
Matches 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.1%;
Best Local Similarity 83.2%;
Matches 371; Conservative 2
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               1 MEQPILIDAYVESASIEKMAS--KSPEPIKIAVANWWGDEEIKEFKKSVIYFIFSQRYTIA 58
                                                                    h 80.3%; Score 1917; DB 2; Length 436;
Similarity 83.1%; Pred. No. 2e-120;
65; Conservative 20; Mismatches 34; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHQNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFQPLLDAYTDSTRLDETDYK--PPLNIALANWWPLDKRESKGFRRFILYFILSQRYTIT 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437
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LHQNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDR 118

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A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are close A;Reference number: Z22749; MUID:99453293; PMID:10521656
A;Accession: T44327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein wbfL [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44327
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A; Residues: 1-346 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
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ILAFFKTILE 340
                                                                                                                        YPSYKGM-VEHKKPIMAQYKFSICYENAKDIPGYITEKIFDSFFAGCVPVYWGANNVT-D
                                                                                                                                             GWDKYRF--TGPILIRAMN----
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                                       FIPENTFIDKRNFSNYB----DLYLYLKNMPDGEYLKYL-ENIENYLNSE----QSLQFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELSONTTFKIYRKAYOKSL 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 193; DB 2;
24.8%; Pred. No. 1.2e-05;
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                                                                      C;Accession: F96533

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, X.Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

R;A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
T18497
hypothetical protein C0780w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18497
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                        probable fucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
  A;Cross-references: UNIPROT:Q9FX97; UNIPARC:UPI000000BD87; GB:AE005173; NID:g10120428;
                    A; Molecule type: DNA
A; Residues: 1-513 <STO>
                                                              A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-2657 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z18935
A;Accession: T18497
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 NHPNLCAV-VNDESDPLKRGVV-----SFVASNANAPMRNAFYDALNSIBPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYDDLRVNYDDLRVNYDDLRVNYDDLRVNYER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYKNILKYIYLDYD--NFLNLNNVYTMRIDESLIID-IAFLGTHTMGCNKQLRNKQDDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLFLEHQN----IYKK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLLELSONTSFKIYRK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYDDDKSNYDDDKSNYDDDKSNYDDDKSNYDDDNKYYDRVHKSGNFLCDDIYKNEMLFNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSF-MWECDLDEPLASIDDLRV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPSVAK----DFNPKEFVNVHDF--NNFDEA--IDYIKYLHTHPNAYLDMLY----EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EGFVQTVVQ 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.7%; Score 160.5; DB 24.9%; Pred. No. 0.028; tive 48; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNKNNYGDNNNNYGDYNNNYDDNRSNYDDDKS
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A; Gene: F14J22.8
A; Map position: :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%; Score 144; DB 2; Length 525; Best Local Similarity 19.3%; Pred. No. 0.04; Matches 107; Conservative 76; Mismatches 176; Indels 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Cross-references: UNIPROT:Q9YVU7; UNIPARC:UPI00000F556B; EMBL:AF063866; NID:g4049647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 NDESDPLKRG--VVSFVASNANAPMRN---AFYDALNSIEPVTG--------
                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                      148
315
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                                                                                                                                                                                                                                                      NSLYTLKKPSHQFKENHPNLCAVVNDESDPLKRGVVSFVASNANAPMRNAFYDALNSIEP
                                                                                                                                                                                                                                                                                                                                                                DKISKNYKLIIHNLL---ROIMNSTDLKEYI----NNIINIDNYKNLSDYIIN----KFW 105
                                                                                                                                                                                                                                                                                                                                                                                                  QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNF----NLFDYAIGFDELDFR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                         LYTPIMNNLIEKYGIDKIFN-----NVCITN------NSYFYILLIEMQNYDIY 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH
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                                                                                                                                                                                                                                                                                                                             DRYLRMP-----SPYKLKD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YENPLNALDGKAYFYQDLSFKKILAFFKTILE------
                                                                       NGFVTHNÍTÍMTYLFĞYKILRQDLLKELFATIKNIPIELSGIISDLLINKNYTAIDETLN
                                                                                                                                                                              VTGGGSVKNTLGYNVKNKSEFLSQ---YKFNLCFENSQGYGYVTEKILDAYFS-----
                                                                                                                                                                                                                     LAISILTNDDABIDITFDNLLEIINND-----RSIFSYINTN------YYPLFKS---
                                                                                                                                                                                                                                                                                           DKVYNVPPSNINIDNIKNINVSSLLSKVVTYKYYD-----PNKVTEFLIFTYYSKKD
HDE--PKITYEIGQINVTSENVYNNYINVIESIAKKPFEPKGYPYNFDVDINKLKFNKKF
                                FDEAIDYIKYLHTHPNAYLDMLYENPLNALDG------KAYFYQ-DLSFKKI---LAF
                                                                                                         ----HTIPIY---WGSPSVAKDFNP----
                                                                                                                                             -SLK-TIEYKFKVSDSNLDPGYLWKSRESFENLKNDGY-AKNFNDVFFSILYSYIR
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                                                                                                        -KEFVNVHDFNN
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[390587]

[1poprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)

[1c] Species: Mycoplasma pulmonis

[c] Species: Mycoplasma pulmonis

[c] Accession: G90587

[c] Accession: G90587

[c] R; Chambaud, I; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

[Rucleic Acids Res. 29, 2145-2153, 2001

[A] Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmon, P.; Moscession: G90587

[A] A; Accession: G90587

[A] A; Accession: G90587

[A] A; Accession: G90587
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A; Residues: 1-789 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 142.5; DB 2;
Local Similarity 21.4%; Pred. No. 0.087;
Nes 107; Conservative 76; Mismatches 174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 YDSKVILLTSENPSSINSKDFKNNLNKAKKIEVFLKEKN-YLNNENKLSSYSLKAMDFYY 194
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   FAYNQVIQL-IKSIHPSLKP
                                                                                                                                                                                                                                                F-KENHPNLCAVVNDESDPLKRGVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLMRDKLSDLSIRKDMNISLKNNEINRK-WNLKNKLSLYKINDEDLFDKNNYDNQKNSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIGFDEL-DFRDRY-LRMPLYYDRLHHKAESVNDTTSPYKLKDNSL-----YTLKKPSHQ 159
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                                                                                                    DDLR-----VNYDDLRVNYDDLRVNYDDLRVNYBBLLQNASPLLBLSQN-TSF 426
                                                                                                                                               HSYANDMILIFGKUNQTUNYNKLYDAYYHLUSFTSFLKKESIUB---NIIDQREKFYLFK
                                                                                                                                                                        -----KILAPFKTILEN-----DTIYHKSS-TSFMWECDLDEPLASIDDLRVNY----
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                                     KIYRKAYQKPIKNPYPYCAP
                                                                         DDQNNILKSKNFEKIKKNLNHLLDNF--
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                                                                           --INQNNIKGNFEWQI----PVYEKAINQEKY
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C;Accession: C97832
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P. Science 293, 2093-2098, 2001
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                         alpha-(1,3)-fucosyltransferase homolog RC1059 [imported] - Rickettsia conorii C;Species: Rickettsia conorii C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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A;Reference number: Z16556; MUID:98054002;
A;Accession: T09079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E. Cell 91, 593-603, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable chloroquine resistance protein CG2 (strain 7G8) - malaria parasite C;Species: Plasmodium falciparum C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C;Accession: T09079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
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;Keywords: toxin resistance
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96; Conservative
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                                                                                                                                                                                                                                                                                                             EEDAWFYCLQKKKKINGDDNKMNGDNKMNGDNKMNGDNKMNGDNKMNGDNKMNG 2298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVEDNKEENIKOLKYKKLKTNE----GEKVDNEFIQVTDNNIIEINPKKKTSTQNEEQPN
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                                                                                                                                                                                                                                                                                                                                                   -----RVNYDDLRVNYD-----
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19.5%; Pred. No. 0.45;
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54002; PMID:9393853
                                                         Fournier, P.B.; Barbe,
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                   Rickettsia
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                   prowazekii
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RESULT 13
T18438
hypothetical protein
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alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mouse
N;Alternate names: ELAM-1 ligand fucosyltransferase homolog
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57596
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A57596
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <KUR>
A;Cross-references: UNIPROT:Q92GR3; UNIPARC:UPI00000CBFA7; GB:AE006914; PIDN:AAL03597.1;
C;Genetics:
C;Genetics:
A;Gene: RC1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-433 <GER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Gersten, K.M.; Natsuka, S.; Trinchera, J. Biol. Chem. 270, 25047-25056, 1995
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                                                                                                                                                                                                                                                                                             83 SYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLKMPLYYDRLHHKAESVNDTTSP 142
                                                                                                                                                                                                                                                                                                                                                                           23 PPPLKIAVANWWGDEEIKEFKKSVLYFIFSORYTIALHONPNEFSDLVFSNPLGSARKIL 82
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LAGAVPVVLG-PDRANYERFVPRGAFIHVDDFPNAASLAAYLLFLDRNVAVY
                                                                                                                                                                                                                                                        NFES-----PSHTPGL
                                       FSHTIPIYWGSPSVA--KDFNPK-EFVNVHDFNNFDEAIDYIKYLHTHPNAY
                                                                                                                                                                                                            YKLKONSLYTLKKPSHQFKENHPNLCAVVNDESDPLKRGVVSFVASNANA-PMRNAFYDA 201
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                                                                                LSRHVSVDVFGRTGPGRPVPAIGL----LHTVARYKFYLAFENSRHVDYITEKLWRNAF 334
                                                                                                                     LNSIEPV----TGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGYVTEKI-LDAY 255
                                                                                                                                                                     Y----GFLYSRSDPTEQPSGLGPQLAR-----KRGLVAWVVSNWNEHQARVRYYHQ 279
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                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 141.5; DB 2;
25.0%; Pred. No. 0.046;
tive 40; Mismatches 112;
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C0415c - malaria parasite (Plasmodium falciparum)

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C;Species: Plasmodium falciparum
(C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18438
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18438
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                      RESULT 14
T09080
                                                                                                                                                                         R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E. Cell 91, 593-603, 1997
A;Title: Complex polymorphisms in an 330 kDa protein are A;Reference number: Z16556; MUID:98054002; PMID:9393853
A;Accession: T09080
                                                                                              A;Molecule type: DNA
A;Residues: 1-2819 <SUX>
A;Residues: 1-2819 <SUX>
A;Cross-references: UNIPROT:015792; UNIPARC:UPI00000785E5; EMBL:AF030693; NID:g2642515;
                                                                                                                                                                                                                                                               probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C;Accession: T09080
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A; Note: C0415c
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C;Genetics:
                                C; Keywords: toxin
                                                                                     A; Experimental source: strain HB3;
                                                                                                                                                         A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-1532 <LAW>
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Best Local :
Query Match
                                                                       Genetics:
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Local Similarity 21.0%;
nes 89; Conservative 5
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                                    resistance
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 5.7%;
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; Pred. No. 0.34;
59; Mismatches 147;
 Score 135;
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                                                                                       Honduras
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 Length 2819;
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A;Accession: H82943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: H82943
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                         A;Genetic code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000013913A; GB:AE002102; GB:AF222894; NID:g6898967; A;Experimental source: serovar 3; biovar 1
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A; Residues: 1-747 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein UU030 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKKSVLYFIFSQRYTIA-----LHQNPNBFSDLVFSNPLGSARKILSYQNAKRVFYTGEN
                                                                                IGFDELD-----FRDRYLRMPLY-YDRLHHKAESVNDTTSPYKLKDNSLYTLK--
                                                                                                                                                                                                              EKILDKN----DYBILMMAANDNDGTLGINIYIKTTKQS--YLINTKPVFLTDKQN-NYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TS----FMWECDLDEPLASIDDLRVNY--DDLRVN------YDDLRVNYDD--
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-----KPSHQFKENHPNLCAVVNDESDPLKRGVVSFVASNANAPMRNAFY---DALN
                                        IGYSEFGSDVQKRLENAFKIRYDEQNIYQINSPQILAKETKTLTSYIDKKTNNNYSINIE 261
                                                                                                                                                                                                                                                                                                                                                                                           SGC3
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                               5.6%; Score 134.5; D
20.7%; Pred. No. 0.28;
ative 77; Mismatches
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2; Mismatches
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### **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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1 MFQPILIDAYVESASIEKWASKSPPPLKIAVANWWGDEBIKEFKNSVLYFILSQRYTITLH
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;
Ge Z., Chan N.W.C., Patico M.M., Taylor D.B.;
"Cloning and heterologous expression of an alphal,3-fucosyltransferase gene from the gastric pathogen Helicobacter pylori.";
J. Biol. Chem. 272:21357-21363(1997).
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:tucosyltransferase activity; IEA.
GO; GO:001677; F:transferase activity, transferring glycosyl.
GO; GO:001677; F:transferase activity, transferring glycosyl.
InterPro; IPR001503; Glyco trans 10.
FANTHER; FTHR1929; Glyco trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;
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84.7%; Pred. No. 1.1e-127;
ive 15; Mismatches 26;
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01-JAN-1998, sequence version 1.
07-PEB-2006, entry version 26.
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Name=fucT;
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                 301 KNAYLDMLYENPLNTLDGKAYFYQNLSFKKILAFFKTILENDTIYH--DNPFIFCRDLNE 358
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016757; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016486; P:protein amino acid glycosylation; IEA.
InterPro; IPR011503; Glyco_trans 10.
InterPro; IPR011503; Glyco_trans 10: 1.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 476 AA; 55927 MW; 32BFFDBBD36E1F74 CRC64;
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Distributed under the Creative Commons Attribution-NoDerivs License
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STRAIN=26695 / ATCC 700392;
STRAIN=2739467; PUDMed=9252185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Watthey J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C., Watthey L., Wallin B., Hays W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
SOGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTH
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
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                                                                                                                                                                                                  YDDLRVNYDDLRVNYERLLQNASPLLELSQNTSFKIYRKAYQKPI 437
                                                                                                                                                                                                                     YDDLRVNYDDLRVNYERLLSKATPLLELSQNTTSKIYRKAYQKSL 463
                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998, integrated into UniProtKB/TrEMBL
01-JAN-1998, sequence version 1.
07-FEB-2006; entry version 25.
                                                                                                                                                                                                                                                                                                                                                                                                 Fucosyltransferase.
OrderedLocusNames=HP0651; ORFNames=HP_0651;
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PIR; C64601; C64601.
TIGR; HP0651; -.
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X MEDLINE=97394647; PUMAGE=9252185; DOI=10.1038/41483;

X MEDLINE=97394647; PUMAGE=9252185; DOI=10.1038/41483;

A Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Kirkness B.F., Pougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., A Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., A Hickey E.K., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Praser C.M., Venter J.C.;

The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                            RGVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFE
                                                                                                                                                 LEMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLK
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GO: GO:0008417; F:fucosyltransferase activity; IEA.
GO: GO:0008417; F:transferase activity, transferring glycosyl.
GO: GO:00167486; F:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTRR11929; Glyco_trans_10.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 425 AA; 49329 WW; 1182AF180D124A34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998, integrated into UniProtKB/TrEMBL 01-JAN-1998, sequence version 1. 07-FBB-2006, entry version 24.
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OrderedLocusNames=HP_0379;
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PIR; C64567; C64567.
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PANTHER, PTHR11929; Glyco_trans_10; 1.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;
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Q9ZKD7;
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                                                               HONPINEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRY
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                                                  1 MPQPLLDAYVESASIEKMASKS-PPPLKIAVANWWGDEEIKBFKKSVLYPIFSQRYTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSZLI3 HELPU PRELIMINARY; PRT; 454 AA.
09ZLI37
01-MAY-1999, integrated into UniProtKB/TrEMBL.
01-MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA (1,3)-FUCOSYLTRANSFERASE.
Name=fucT; ORFNames=jhp 0596;
Helicobacter pylori J99 (campylobacter pylori J99).
Bacteria; Proteobacteria Epsilonproteobacteria; Campylobacterales;
                         29;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 82.6%; Score 1972.5; DB 2; Length 425;
                         24; Indels
            Pred. No. 8.7e-121;
9; Mismatches 24;
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GO; GO:0006486; P:protein amino acid
InterPro; IPR001503; Glyco_trans_10.
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            Best Local Similarity 85.8
Matches 376; Conservative
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357 NEPLVAIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLLVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLR
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MEDLINE=99120557; PubMed=992362; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Garla B.C., deJonge B.L., Carmel G.,
Tummino P.J., Carmel G.,
Tummino P.J., Carmel G.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
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Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
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     454;
     DB 2; Length
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
82.1%; Score 1959.5; DB 2;
83.2%; Pred. No. 6.7e-120;
tive 25; Mismatches 37;
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21-FEB-2006, entry version 23.
ALPHA-(1,3)-FUCOSYLTRANSFERASE.
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NUCLEOTIDE SEQUENCE.
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Q9L8S4;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
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                                                                                                                                                                                              KRGVVS FVASNANA PMRNA FYDALNS I EPVTGGGSVKNTLGYNVKNKS EFLSQYKFNLCF
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                                                                                                                                   MFQPLLDAYVESASIEKMAS--KSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIA
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                          20;
GO; GO:0016757; F:transferase activity, transferring glycosyl. GO; GO:0006486; P:protein amino acid glycosylation; IEA. InterPro; IPR001503; Glyco_trans_10. PANTHER; PTHR11929; Glyco_trans_10; 1. Complete proteome; Glycosyltransferase; Transferase. SEQUENCE 436 AA; 50699 MW; IDB2066AB98FA61E CRC64;
                                                                                  Length 436;
                                                                                                           34; Indels
                                                                                Query Match

80.3%; Score 1917; DB 2;
Best Local Similarity 83.1%; Pred. No. 3.8e-117;
Matches 365; Conservative 20; Mismatches 34;
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STRAIN=DSM 6709;
PubMed=16000696; DOI=10.1093/glycob/cwj004;
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ELSQNTTFKIYRKAYQKSL
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Name=fucTIII;
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                     432;
                                                                                                                                                     2; Length
                                                                                                                                                Query Match 79.3%; Score 1894.5; DB 2; Length Best Local Similarity 81.3%; Pred. No. 1.1e-115; Matches 356; Conservative 30; Mismatches 33; Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
GO; GO:0006486; P:protein amino acid glycosylation; IEA
                     InterPro, IPR001503, Glyco_trans_10.
PANTHRS, PTHR11929, Glyco_trans_10; 1.
Glycosyltransferase, Transferase, SEQUENCE 432 AA, 50503 MW; 69D3A32FBD2F12C9 CRC64;
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GO; GO:0006486; P:protein amino
InterPro; IPR002105; Dockerin_1.
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Best Local Similarity 86.4%;
Matches 279; Conservative 15
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Q5L9S6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLH 298
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Distributed under the Creative Commons Attribution-NoDerivs License
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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Bird M.I.;
"Lewis X biosynthesis in Helicobacter pylori. Molecular cloning
EMBL; AP194963; AAF35291.2; -; Genomic_DNA.
GO; GO:0006417; F:tucosyltranaferase activity; IEA.
GO; GO:0006417; F:tucosyltranaferase activity; IEA.
GO; GO:0016757; F:tranaferase activity, transferring glycosyl.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco trans 10.
PANTHER; PTR11929; Glyco_trans 10.
Glycosyltranaferase; Transferase.
SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;
                                                                                                                                                                                                                                                                         21;
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MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
                                                                                                                                                                                                                               DB 2; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDEPLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY-
                                                                                                                                                                                                                           75.9%; Score 1812.5; DB 2; Length
76.2%; Pred. No. 2.8e-110;
iive 33; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ERLLQNASPLLELSQNTSFKIYRKAYQKPI 437
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01-JAN-1998, integrated into UniProtKB/TrEMBL
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07-FEB-2006, entry version 23.
Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-).
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J. Biol. Chem. 272:21349-21356(1997).
                                                                                                                                                                                                                           Query Match 75.9
Best Local Similarity 76.2
Matches 346; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
Abrart V., Lemnard M., Poxton I., Duerden B., Harris B., Quail M.A.,
Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
Line A., Lord A., Norbertczak H., Ormond D., Price C.,
Rabbinowiteben B., Woodward J., Barrell B.G., Parkhill J.;
Extensive DNA inversions in the B. fragilis genome control variable
EMBL; AF006039; AAB93985.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000841; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
FANTHER; PTHA11929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 333 AA; 39154 MW; CFFCBIAC127E0A8C CRC64;
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Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                           16; Indels
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016746; F:transferase activity; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.
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21-JUN-2005, sequence version 1.
07-FEB-2006, entry version 6.
Putative LPS blosynthesis related glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                       Score 1502.5; DB
Pred. No. 3.7e-90;
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Matches 107; Conservative
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                               Best Local Similarity
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Q2IE19;
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Best Local S
Matches 90
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                 Query Match
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                                                                                                                                                                                                                                                                                                            -----LDRKFCSIVVSNNKWADPIRETFFKLLSSY 154
                                                                                                                                                       WWGDEEIKEFKKSVLYFIFSORYTIALHONPNEFSDLVFSNPLGSARKILSYONAKRVFY 92
                                                                                                                                                                                   24 WDGFDTISNPIVDAL----SIQYEVVLSNEP----DYLPYSCFGTSH--LEYDCIK-IMP 72
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BioCyc; HHEP235279:HH1776-MONOMER; -.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0006417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. ..; IEA.
GO; GO:0016757; F:transferase activity, transferase.
GO; GO:0016757; F:transferase.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 359 AA; 42275 MW; BOIB3FBBBC82D463 CRC64;
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                                                                                                                          Gaps
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MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
Suerbaum S., Josenhens C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Weber J., Prosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
"The complete hepaticus.";
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                          63;
                                                                                            DB 2; Length 331;
                                                                                         Query Match
18.5%; Score 442.5; DB 2; Length 3
Best Local Similarity 35.8%; Pred. No. 8.4e-21;
Matches 111; Conservative 42; Mismatches 94; Indels
InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10; 1.
PROSITE; PS000448; CLOS_CELLULOSOME_RPT; UNKNOWN_1.
Complete proteome; Transferase.
SEQUENCE 331 AA; 39181 MW; 679FA409DF8CB864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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01-OCT-2003, sequence version 1.
07-FEB-2006, entry version 12.
17-Dha-1,3-fucosyltransferase.
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                                                                                                                             44 KSVLYFIFSQRYTIALHQNPNBFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNL 103
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                     23 KGKIVALLEQHYELIL---TNKDPDYIFYSCMGFEH--LNY-NKVRIFATGENLRADFNF
                                                                                                                                                                                                                                                       104 FDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKEN
                                                                                                                                                                                                                                                                                                  168 VDKYAFLKEGKFNIAFENSSTNGYITEKLIQAFAAHTIPIYWGDERISLPLDKMGGGINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEPVNVHDFNNFDBAI DYIKYLHTHPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 KNKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVA-----KDFNP
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-2CP-C;
US DOB Joint Genome Institute;
US DOB Joint Genome Institute A., Barry K., Detter J.C., Glavina 'Hammon N., Israni S., Ptluck S., Brettin T., Bruce D., Han C., Tapia R., Gilna P., Kiss H., Schmutz J., Larimer F., Land M., Kyrpides N., Anderson I., Sanford R.A., Ritalahti K.M., Thomas H.S Rirby J.R., Zhulin I.B., Loeffler F.B., Richardson P.;
"Complete sequence of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                  68;
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07-MAR-2006, entry version 1.
Putative LPS biosynthesis related glycosyltransferase.
ORFNames=Adeh 3065
Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaprotechacteria; Myxococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 29.8%; Score 309; DB 2; Length 287; Similarity 29.8%; Pred. No. 3.8e-12; Onservative 54; Mismatches 114; Indels '
      Length 359;
17.5%; Score 419; DB 2; Length 35
31.9%; Pred. No. 3.2e-19;
ive 51; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 AA; 34352 MW; 82CEAB6961E314A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cystobacterineae; Myxococcaceae; Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 KTILEN-----DTIYHKSSTSFMWECDLDE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 DEKLENFLLHIFNQPLEKAYRRGFG--QWRCNIEK 307
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273 FNPKE-FVNVHDFNNFDEAIDYIKYLHTHPNA-YLDMLYENPLNALDGKAYFYQDLSFKK 330
                                                                                                                                          PRELIMINARY;
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 435:43-57(2005).
                                                   331 ILAFFKTILE 340
                                                                            331 -EGFVQTVVQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                         Q54PH9_DICDI
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                          279
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Q54PH9
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                                       141
                                                                                                                              144 KLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKRGVVSFVASNANAPMRNAFYDALN 203
                                                                                                                 WGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTHPNAYLDMLYENPLNALDGKAYFY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 WSDDLVDGVKYIKINY------AHAFPN------CIEKNLTNKKALCVLIA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 GENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTTSPYKLKONSLYTL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 G-NKKPKTTLDPALFSLDLYNEREKAIR---WFEKNH-------IQDFDLYGV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 KKPSHQFKENHPNLCAVVNDESDPLKRGVVSFVASNANAPMRNAFYDALNSIEPVTGGGS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 GWDKYRF--TGPILIRAMN------RVPM-----LPQLAQKILGRS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 YPSYKGM-VEHKKPIMAQYKPSICYENAKDIPGYITEKIFDSPPAGCVPVYWGANNVT-D 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are closely related to those of Vibrio cholerae 022."; Gene 237:321-332(1999).
                             SIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 VRNTLGYNVKNKSEFLSQYKFNLCFENSQGY-GYVTEKILDAYFSHTIPIYWGSPSVAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=99453293; PubMed=10521656; DOI=10.1016/S0378-1119(99)00344-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamasaki S., Shimizu T., Hoshino K., Ho S.-T., Shimada T., Nair G.B.,
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                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IFR001503; Glyco trans 10.
PANTHER; PTHR11929; Glyco trans 10;
SEQUENCE 346 AA; 40359 WW; Z8690BG3FEFFDA7F CRC64;
                                                                                                                                                                                                                                                                                 01-NOV-1998, integrated into UniProtKB/TrEMBL
01-NOV-1998, sequence version 1.
07-EBB-2006, entry version 22.
WbfL protein.
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O87156;
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Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae.
                                                                                                                                                                   QD 325
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                                                                                                                                                                                            SD 261
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STRAIN-AX4;

STRAIN-AX4;

Sugang R., DoI=10.1038/nature03481;

Rubhdei-15875012;

Rubhdei-15875012;

Richinger L., Schleicher G., Rajandream M.A.,

Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu O.,

Sucgang R., Berriman R., Hamlin N., Davies R., Gauder P., Fey P.,

Bankier A.T., Lehmann R., Hamlin N., Davies R., Davie P.,

Pilcher K., Chen G., Saunders D., Sodergren E.J., Davie P.,

Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Rarborcher P., Desany B., Just B., Morio T., Rost R., Churcher C.M.,

Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

Nazny D.M., Mourier T., Pain A., Iu M., Harper D., Lindsay R.,

Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,

Ruchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,

Knights A., Loulseged H., Mungall K.L., Oliver K., Price C.,

Quail M.A., Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D.,

Anders M., Ma J., Kohara Y., Slarg S., Simmonds M.N., Spiegler S.,

Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,

Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,

Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
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PIPENTFIDERNFSNYE---DLYLYLKUMPDGEYLKYL-ENIENYLNSE----QSLQFKS 330
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Distributed under the Creative Commons Attribution-NoDerivs License
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GO; GO:0016020; c:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

InterPro; IPR001503; Glyco.trans 10.

BANTHER; PTHR11929; Glyco.trans 10; 1.

Glycosyltransferase; Golgl stack; Hypothetical protein; Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2005, integrated into UniProtKB/TrEMBL.
24-MAY-2005, sequence version 1.
47-MAR-2006, entry version 5.
Hypothetical protein futt.
Name-futl; ORFNames=DDB0219943;
Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetczoa, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                     389 AA.
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24-MAY-2005,
07-MAR-2006,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             118 R---YLRM-PLYY---DRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAV 170
                                                                                                                                                                                                                                       171 VNDESDPLKRGVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLS 230
97 SSNKIYNNTLKRYNPRQITIGWTMESGGLYRFEGDSNFIISNFNI---TVGYPRVNDFNK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 AIDYIKYLHTHPNAYLDML------YENPLNALDGKAYFYQDLSFKKIL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 QTHIYVPYGPVEYSGSDSYAHSAKFDRIKEIPSK-RNNSIVWIS--SNCWHEDY-----
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Transmembrane.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA
InterPro; IFR01503; Glyco trans 10.
PANTHER; PTHR11929; Glyco trans 10: 1.
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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054PU9

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24-MAY-2005, integrated into UniProtKB/TrEMBL.

24-MAY-2005, sequence version 1.

07-MAR-2006, entry version 5.

Hypothetical protein.

0RFNames=DDB0186041;
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462 AA; 54815 MW; 444843FFBAEF6D77 CRC64;

SEQUENCE

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Sucgang R., Berriman M., Song J. Olsen R., Szafranski K., Xu Q., Sucgang R., Berriman M., Song J. Olsen R., Szafranski K., Xu Q., Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., Ranfort R., Chen G., Saunders D., Sodergren E., Davis P., Rathornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., Rarborther P., Desany B., Just E., Morio T., Rost R., Churcher C., Rarborther P., Desany B., Just E., Morio T., Rost R., Churcher C., Androper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Marzy D., Mourier T., Pain A., Lu M., Harper D., Lindsay R., Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A., Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M., Malker D., Woodward J., Winckler T., Tanaka Y., Sharp S., Simmonds M., Spiegler S., Tivey A., Sharp S., Simmonds M., Spiegler T., Tanaka Y., Sharp S., Simmonds M., Spiegler T., Tanaka Y., Sharp S., Simmonds M., Rohell R., Kay R., Chleicher M., Weinstock G., Rosenthal A., Cox E.C., Millams M., Looris W.F., Barrell B., Kuspa A., Williams V., Dar P.H., Noegel A.A., Barrell B., Kuspa A., The genome of the social amoeba Dictyostelium discoideum."; Nature 0:00 (2005)
                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 FIVUDSFGKCLKNMPTSNFLSRGSGDPPERKRLFITRYKFTIVFENSICKDYVSEKVLDA 340
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 YPIFSQRYTIALHQNPNE-----FSDLV--FSNPLGSARKILSYQNAKRVFYTGENEVP
                                                                                                                                                                                                                                 131 YYIVRKPY-----YPNOKLDMBIWSDYIVDFBAP----KKKLSSRNVPRTLISMBPO-P
                                                                                                                                                                                                                                                                                                                             100 N-----FNLFDYAIGFD-BLDFRDRYLRMPLYYDRLHHKAESVNDTTSPYKLKDN-
                                                                                                                                                                                                                                                                                                                                                                           180 NRTCEFDKDCFEFFNFKVSFESQSDIR------MGFD-----TPSSSAYKLYNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 SLYTLKKPSHQFKENHP----NLCAVVNDESDPLKRGVVSFVASNANAPMRNAFYDALNS
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                                                                                   63;
Length 462;
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Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
                                                                                   Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR01330; ConA like subgrp.
InterPro; IPR001503; Glyco_trans_10.
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
8.0%; Score 191.5; DB 2; 25.6%; Pred. No. 0.00034;
                                                                               50; Mismatches 105;
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Query Match
Best Local Similarity 25.6%
Matches 75; Conservative
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                                                                                                                                                                                           Query Match 7.6%; Score 182; DB 2; Length 665; Best Local Similarity 21.6%; Pred. No. 0.0022; Matches 100; Conservative 72; Mismatches 167; Indels 124; Gaps
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                     Hypothetical protein.
SEQUENCE 665 AA; 76223 MW; D42588B008EBDB46 CRC64;
PANTHER; PTHR11929; Glyco_trans_10; 1.
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/EMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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4440 3722 302 302 306 136 4433 4433 365 365 365 365		ESULT 1 Sequence 1, Application US/0909231 Patent No. 63993737 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Taylor, Diane E. APPLICANT: Ge, Zhongming TITLE OF INVENTION: ALPHA-1, 3-FU FILE REFERENCE: 07254/049001 CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 1997-06-05 EARLIER APPLICATION NUMBER: US EARLIER PILING DATE: 1997-06-05 SOFTWARE: FASESO ID NOS: 22 SOFTWARE: FASESO ID NOS: 22 SOFTWARE: FASESO ID NOS: 22 SOFTWARE: PASE ID NOS: 22 SOFTWARE: PASESO ID NOS: 23 SOFTWARE: PRI ORGANISM: Helicobacter pylori	쑱	VESAS1	VFSNPI 	HKAES        HKAES	ANAPME  - - - PNAPIF	CLDAN CLDAN	ENPLANT
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Patent No. 6534298

GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongwing
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/733,524A
CURRENT FILING DATE: 1200-12-07
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PRILING DATE: 1998-06-05
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ. ID NOS: 27
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RESULT 3 US-10-189-977A-1

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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Canoming
TITLE OF INVENTION: PUCCSTLETC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION NUMBER: US/09/733,524
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
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87.4%; Score 2086; DB 2;
Best Local Similarity 87.4%; Pred. No. 1.6e-189;
Matches 394; Conservative 15; Mismatches 26;
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Patent No. 7029891

GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/392,098A
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1, Application US/10189977A
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US-10-189-977A-1
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US-10-392-098A-1
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RESULT 6
US-10-189-977A-7
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APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Go, Zhonghing
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: FUCOSYLITRANSPERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-04902.
CURRENT APPLICATION NUMBER: US/09/733,524A

CURRENT FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: US 69/092,315

PRIOR APPLICATION NUMBER: US 60/048,857
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: H. pylori strain NCTC11639
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpPucT)
US-10-392-098A-1
                                                                                                                                                                                                                                                                                                                                                                  Length 464;
                                                                                                                                                                                                                                                                                                                                                             Query Match 87.4%; Score 2086; DB 3; Length 4. Best Local Similarity 87.4%; Pred. No. 1.6e-189; Matches 394; Conservative 15; Mismatches 26; Indels
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419 YERLLSKATPLLELSQNTTSKIYRKAYQKSL 449
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             PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR FILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-06-05
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PILING DATE: 1988-06-05
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 464
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Patent No. 6534298
2003-03-17
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Helicobacter pylori
 CURRENT FILING DATE:
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US-09-733-524A-7
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GENERAL INCRMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: WUCLEIC ACIDE ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REPRENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT APPLICATION NUMBER: US/09/733,524

PRIOR FILING DATE: 1009-12-07

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

NUMBER OF SEQ ID NOS: 27
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87.1%; Score 2079; DB 2;
Best Local Similarity 84.7%; Pred. No. 7.9e-189;
Matches 394; Conservative 15; Mismatches 26;
                        NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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                                                                                                                         ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-7
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; ORGANISM: Helicobacter pylori
US-10-189-977A-7
PRIOR FILING DATE: 1997-06-06
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                                                                                               QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL
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                                                                               1 MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH
                                          Gaps
                                        30;
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OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
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84.7%; Pred. No. 7.9e-189;
tive 15; Mismatches 26; Indels 3
Length 478;
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                                        26; Indels
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APPLICANT: G., Zhongming;
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase;
FILE REFERENCE: 017398-0004200S
CURRENT APPLICATION NUMBER: US/10/1392,098A
CURRENT FILING DATE: 2003-03-17
PRIOR PLILING DATE: 2002-04-09
PRIOR PLILING DATE: 1997-06-06
PRIOR PLILING DATE: 1997-06-06
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 09/733,524
PRIOR FILING DATE: 1098-06-05
PRIOR APPLICATION NUMBER: US 09/733,524
PRIOR PLILING DATE: 1098-06-05
PRIOR APPLICATION NUMBER: US 09/733,524
PRIOR PLING DATE: 2000-12-07
SOFTWARE: PATENTIN VO: 2.1
LENGTH: AND
Query Match

87.1%; Score 2079; DB 2;
Best Local Similarity 84.7%; Pred. No. 7.9e-189;
Matches 394; Conservative 15; Mismatches 26;
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ORGANISM: Helicobacter pylori
FEATURE:
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Best Local Similarity 84.73 Matches 394; Conservative

Gaps

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61 ONPNEFSDLVFSNPLGSARKILSYONAKRVFYTGENEVPNFNLFDYALGFDELDFRDRYL 120
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1 MFQPLLDAYVESASIEKWASKSPPPLKIAVANWWGDEEIKEFKNSVLYFILSQRYTITLH
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Patent No. 6399337
GENERAL INFORMATION
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: US/09/092,315
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SSOTTWARE: FastSEQ for Windows Version 3.0
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84.5%; Pred. No. 2.9e-188;
tive 15; Mismatches 27;
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Matches 393; Conservative
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US-09-092-315-7
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, ORGANISM: Helicobacter pylori
US-09-733-524A-8
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Best Local Similarity 86.5%
Matches 384; Conservative
                      RESULT 10
US-09-733-524A-8
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241 SQGYGYVTEKIIDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDBAIDYVRYLHTH 300
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                                                                                                                                                                      419 YDDLRVNYDDLRVNYERLLSKATPLLELSONTTSKIYRKAYOKSL 463
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Patent NO. 639937
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION:
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1990-06-05
EARLIER FILING DATE: 1990-06-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE FEASES (for Mindows Version 3.0)
SEQ ID NO 8
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; ORGANISM: Helicobacter pylori
US-09-092-315-8
                                                                                                     PLASIDDLRV-
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US-09-092-315-8
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Sequence 8, Application US/09733524A

| Sequence 8, Application US/09733524A
| Patent No. 6534296
| GENERAL INPOWEMATION:
| APPLICANT: Taylor, Diane E.
| APPLICANT: Taylor, Diane E.
| APPLICANT: Taylor, Diane E.
| TITLE OF INVENTION: WOCKLET AND EXPRESSION SYSTEMS FOR MAKING AND ITILE OF INVENTION: EXPRESSING THEM (amended)
| TITLE OF INVENTION: EXPRESSING THEM (amended)
| FILE REFREENCE: 07254-049002
| FILE REFREENCE: 0726-0409733,524A
| CURRENT FILING DATE: 1998-06-05
| PRIOR PILING DATE: 1998-06-05
| PRIOR PILING DATE: 1998-06-05
| NUMBER OF SEQ ID NOS: 27
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 8, Application US/10189977A

Sequence 8, Application US/10189977A

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: FUCCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
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86.5%; Pred. No. 4.7e-188;
tive 27; Mismatches 24;
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Query Match
Best Local Similarity
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; Batent No. 7029891
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Taylor, Diane E.
; APPLICANT: Taylor, Diane E.
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
; FILE REPERBUCE: 017398-000420US
; CURRENT APPLICATION NUMBER: US/10/120,319
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR APPLICATION NUMBER: US 60/048,857
; PRIOR PALLIGATION NUMBER: US 60/048,857
; PRIOR PILLING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                86.7%; Score 2070.5; DB 2
86.5%; Pred. No. 4.7e-188;
tive 27; Mismatches 24;
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/189, 977A
CURRENT FILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-012-07
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1999-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTESEQ FOR Windows Version 4:0
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Best Local Similarity 86.5'
Matches 384; Conservative
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                                                                                                                                                                                                                                                                                                                                                Query Match 86.7%; Score 2070.5; DB 3; Length 454; Best Local Similarity 86.5%; Pred. No. 4.7e-188; Matches 384; Conservative 27; Mismatches 24; Indels 9;
                                                                                                                                                                                                                                     ) OTHER INFORMATION: H. pylori strain NCTC11637
) OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-8
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US-09-092-315-5

Sequence 5, Application US/09092315

Sequence 6, Application US/09092315

Patent No. 6399337

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming

TILE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE

FILE REFERENCE: 07254/049001

CURRENT FILING DATE: 1998-06-05

EARLIER APPLICATION NUMBER: US/09/092,315

EARLIER APPLICATION NUMBER: US 60/048,857

BARLIER APPLICATION NUMBER: 1997-06-06

NUMBER OF SEQ ID NOS: 22
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US-09-092-315-5
                                                                                                                                                            TYPE: PRT
ORGANISM: Helicobacter pylori
                   PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
  PRIOR APPLICATION NUMBER: US
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Sequence 5, Application US/10189977A Patent No. 6962806
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US-10-189-977A-5
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US-10-189-977A-5
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Batent No. 6534298

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: WIGHER CAIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REPRENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/09/733,524A

CURRENT PILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/048,857

PRIOR PILING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastsEQ for Windows Version 4.0

SOFTWARE: FastsEQ for Windows Version 4.0
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31; Gaps
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28; Indels
13; Mismatches
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; ORGANISM: Helicobacter pylori
US-09-733-524A-5
394; Conservative
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Matches 394; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
CURRENT PLING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US 60/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FRRESEQ FOR Windows Version 4.0
                                                                                                                                                                                       240 NSQGYGYVTEXILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHT 299
241 NSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDXIKYLHT 300
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86.2%; Score 2058.5; DB 2;
Best Local Similarity 84.5%; Pred. No. 7e-187;
Matches 394; Conservative 13; Mismatches 28;
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Db 241 NSQCYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYLHT 300 QY 300 HPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENPTIYHKSSTSFMWBCDLD 359
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: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-130-319-1

US-10-392-098-1

US-10-392-098-1

US-10-189-977-7

US-10-189-977-7

US-10-189-977-8

US-10-189-977-8

US-10-189-977-8

US-10-189-977-8

US-10-189-977-8

US-10-189-977-5

US-10-189-977-5

US-10-189-977-5

US-10-189-977-2

US-10-189-977-2

US-10-189-977-2

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US-10-189-977-6

US-10-189-977-6
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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8558, Ap
66, Appl
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100.0%; Pred. No. 9.2e-191;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Ocovernors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
US-09-733-524-16
US-10-764-212-4
US-10-135-977-8559
US-10-130-319-3
US-10-189-977-3
US-10-189-977-3
US-10-189-977-3
US-10-764-212-18
US-10-764-212-20
US-10-764-212-20
US-10-120-319-13
US-10-120-319-13
US-10-764-212-68
US-10-764-212-68
US-10-764-212-68
US-10-764-212-75
US-10-764-212-74
US-10-764-212-74
US-110-764-212-74
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                                                                                                                                                                                                                                                                                          Sequence 16, Application US/10764212
Publication No. US20050164338A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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Best Local Similarity
  JS-10-764-212-16
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GVVSFVASNANAPMRNAFYDALNSIEPVTGGGGSVRONTLGYNVRNKSEFLSQYKFNLCFEN

GVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN

181

301 PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLDE 360

241

241 SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTH

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US-10-392-098-1
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359 PLYTIDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRVN
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361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDLRVNYERLLQNASPLIEL
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                                                    PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEL
                                                                                                                                                                                                                                                                             APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLITRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT PILING DATE: 2002-04-09;
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PASISEQ for Windows Version 3.0
LENGTH: 464
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87.4%; Score 2086; DB 4; Length 464;
Best Local Similarity 87.4%; Pred. No. 1.7e-165;
Matches 394; Conservative 15; Mismatches 26; Indels 10
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                                                                                                                     421 SONTSFKIYRKAYOKPIKNPYPYCAP 446
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Publication No. US20020164749A1
GENERAL INFORMATION:
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; ORGANISM: Helicobacter pylori
US-10-120-319-1
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US-10-120-319-1
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RESULT 3

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Sequence 1, Application US/10392098
Publication No. US20030166212A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCGSULTRANSFERASS AND EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/392,098
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/733,524A
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                                                                         APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REPERBICE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 1908-06-05
PRIOR APPLICATION NUMBER: US/09/092,315
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PRAESEQ FOR WINDOWS Version 3.0
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Best Local Similarity 87.4%; Pred. No. 1.7e-165;
Matches 394; Conservative 15; Mismatches 26;
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Sequence 1, Application US/10189977
Publication No. US20030166211A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
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, ORGANISM: Helicobacter pylori
US-10-392-098-7
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Sequence 7, Application US/10392098

Publication No. US20030166212A1

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: FUCOSYLIRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/09/733,524A

PRIOR PILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR PILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                   Length 464;
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-1
                                                                                                                                    LENGTH: 464
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APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT PILING DATE: 2002-04-09
FILE APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
Length 478;
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-10-120-319-7
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GENERAL INFORMATION:
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: FUCOSYLITANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: FUCOSYLITANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM
FILE REFERENCE: 07254/049002
CURRENT PILING DATE: 2000-12-14
FRIOR APPLICATION NUMBER: 09/092,315
FRIOR APPL
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359 PLVTIDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRINYDDLRVNYDDLRVNYDDLRIN 418
241 IQGYGYVTEKIIDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLHTH 300
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86.8%; Score 2073; DB 3; Length 50;
Best Local Similarity 87.1%; Pred. No. 2.3e-164;
Matches 393; Conservative 15; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09733524
Patent No. US20020068347A1
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241 TQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYIKYLHTH 300
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86.8%; Score 2073; DB 4; Length 478;

Best Local Similarity 84.5%; Pred. No. 2.1e-164;

Matches 393; Conservative 15; Mismatches 27; Indels 30;
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APPLICANT: Taylor, Diane B.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REPERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
FRIOR PILING DATE: 1998-06-05
FRIOR PILING DATE: 1998-06-05
FRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10189977
Publication No. US20030166211A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
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                                                                                                   Sequence 8, Application US/10120319; Sequence 8, Application No. US20020164749A1; Sequence 10. US20020164749A1; Publication No. US20020164749A1; Publication No. US20020164749A1; Sebilication No. US20020164749A1; Total Control Number: US/10/120,319; CURRENT FILING DATE: 2002-04-09; PRIOR PEPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/092,315; PRIOR PILING DATE: 1998-06-05; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06; NUMBER OF SEQ ID NOS: 22; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NOS: 22
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86.5%; Pred. No. 3.2e-164;
ive 27; Mismatches 24; Indels 9;
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APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
                419 YERLLSKATPLLELSQNTTSKIYRKAYQKSL 449
407 YERLLQNASPLLELSQNTSFKIYRKAYQKPI 437
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Publication No. US20030166211A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Helicobacter pylori
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Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 454
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US-10-189-977-8
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GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: WUCLEIC ACIDE ENCODING ALPHA-1,3
TITLE OF INVENTION: PUCOSTITRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07224-049002
CURRENT APPLICATION NUMBER: US,10/392,098
CURRENT APPLICATION NUMBER: US,09/7733,524A
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
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                CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US/09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPLLELSQNTSFKIYRKAYQKPI 437
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Publication No. US20030166212A1
                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
FILE REFERENCE: 07254/049001
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Matches 384; Conservative
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DB 3; Length 454;

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patent No. US20020068347A1

GENERAL INFORMATION:
APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
TITLE OF INVENTION: WIGHER ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM
TITLE OF INVENTION: EXPRESSING THEM
PILE OF INVENTION: EXPRESSING THEM
PRICE OF INVENTION NUMBER: 09/092,315
PRIOR PILING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LEAGURE OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LEAGURE OF SEQ ID NO 18
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                                                                                                         Length 454;
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                                                                                                             DB 4;
                                                                                                         Query Match

86.7%; Score 2070.5; DB 4,
Best Local Similarity 86.5%; Pred. No. 3.2e-164;
Matches 384; Conservative 27; Mismatches 24;
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ORGANISM: helicobacter pylori fucosyltransferase
FEATURE:
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; OTHER INFORMATION: Strain 11637 from NCTC11637
US-09-733-524-18
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                                  ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-8
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SEQ ID NO 8
LENGTH: 454
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Sequence 15, Application US/09733524

Sequence 15, Application US/09733524

Sequence 15, Application US/09733524

GENERAL INFORMATION:

APPLICANT: The Governmers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: WICKLER AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM

FILE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

FILE OF INVENTION NUMBER: US/09/733,524

CURRENT APPLICATION NUMBER: US/09/2,315

PRIOR APPLICATION NUMBER: 60/048,857

PRIOR APPLICATION NUMBER: 60/048,857

PRIOR APLICATION NUMBER: 60/048,857

PRIOR APLICATION NUMBER: 60/048,857

PRIOR APLICATION NUMBER: 60/048,857

SPRIOR PILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Fastered for Windows Version 4.0

SEQ ID NO 15.
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                                                        25; Indels
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ORGANISM: Helicobacter pylori fucosyltransferase
86.5%; Score 2064.5; DB
86.3%; Pred. No. 1e-163;
tive 27; Mismatches 2
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OTHER INFORMATION: Strain 26695A
  Query Match
Best Local Similarity 86.3%
Matches 383; Conservative
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Matches 394; Conservative
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241 NSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYLHT 300
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APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US/09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
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SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 5, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
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US-10-189-977-5
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MPQPLLDAFIESASIEKMVSKSPPPPLKIAVANWWGDEBIKEFKKSVLYFILSQRYAITL 60
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                                 RGVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFE
                                                                                                        LRMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLK
                                                                                                                                                                                                                                                   NSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHT
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APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

PERENCHIS OF Zhonguing
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE

FILE REFERENCE: 07254/049001
CURRENT APPLICATION WUMBER: US/10/120,319

CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/092,315

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05

PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PARENCE WINDOWS VERSION 3.0

LENGTH: 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 NYDDLRVNYDDLRVNYDRLLQNASPLLELSQNTTFKIYRKAYQKSL 464
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Publication No. US20020164749A1
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ORGANISM: Helicobacter pylori
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Best Local Similarity 84.54
Matches 394; Conservative
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US-10-120-319-5
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Gaps

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Search completed: August 11, 2006, 19:53:05 Job time : 109.675 secs

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#### November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions rapbm (Published\_Applications\_AA\_New).

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Sequence 5128, Ap
Sequence 5127, Ap
Sequence 44967, A
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52598, A
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3, Appli
48384, A
21, Appl
8, Appli
27, Appl
25, Appl
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4748, Ap
                                                                                       August 11, 2006, 19:47:49; Search time 16.9493 Seconds (without alignments) 1771.230 Million cell updates/sec
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/EMC Celerra SIDS3/prodata/2/pubpaa/US06_NEW_PUB.pep:*
/EMC Celerra SIDS3/prodata/2/pubpaa/US07_NEW_PUB.pep:*
/EMC Celerra SIDS3/prodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/prodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/prodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC Celerra SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep:*
/EMC Celerra SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep:*
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2388
1 MFQPLLDAYVESASIEKMAS......KIYRKAYQKPIKNPYPYCAP 446
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GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-953-349-5127
US-10-449-902-244967
US-11-197-712-284
US-10-649-902-52598
US-10-537-642-9
US-10-537-642-9
US-10-537-642-24
US-10-537-642-24
US-10-537-642-24
US-10-537-642-24
US-10-537-642-8
US-10-537-641-175
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA New:
                                                                                                                                                                                                                                                                239914 seqs, 67312017 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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2133
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Perfect score:
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                                                                                          Run on:
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Sequence 86, Appl	2	Sequence 171, App	_		Sequence 110, App	Sequence 1894, Ap	Sequence 80, Appl	Sequence 112, App	Sequence 4, Appli	Sequence 257, App	Sequence 5110, Ap	Sequence 11, Appl	Sequence 13, Appl	Sequence 14, Appl	Seguence 18, Appl	Sequence 75786, A	Sequence 75785, A	Sequence 3528, Ap	Sequence 36, Appl
US-10-527-411-86	US-10-527-411-90	US-10-527-411-171	US-10-527-411-173	US-10-527-411-104	US-10-527-411-110	US-10-471-571A-1894	US-10-527-411-80	US-10-527-411-112	US-10-126-915-4	US-10-505-928-257	US-10-471-571A-5110	US-10-521-401A-11	US-10-521-401A-13	US-10-521-401A-14	US-10-537-642-18	US-11-056-355B-75786	US-11-056-355B-75785	US-10-471-571A-3528	US-11-192-046-36
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4.4	4.	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1
104	104	103	103	103	103	102.5	102.5	102.5	102	101.5	100.5	100.5	100.5	100.5	100	98.5	98.5	98.5	98.5
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#### ALIGNMENTS

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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5128, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 DYIKYLHTHPNAYLDML---YENPLNALDGKAYFYQDLSFKKILAFFKTILE----- 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 FNLCPENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNP--KEFVNVHDFNNFDEAI 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 148.5; DB 6; Length 302;
25.8%; Pred. No. 0.00015;
trive 34; Mismatches 78; Indels 35
                  Sequence 5129, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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184 FKKRPCKCSRGGSDTVYH 201
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Matches 51; Conserv
US-10-953-349-5129
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US-10-953-349-5128
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APPLICANT: Dunas Milne Edwards, Jean Baptiste
APPLICANT: Dunas Milne Edwards, Jean Baptiste
APPLICANT: Dunas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret. Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.U54.CIP
CURRENT APPLICATION NUMBER: US/11/197,712
CURRENT APPLICATION NUMBER: US/09/876,997
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR PLILING DATE: 2000-03-06
PRIOR PLILING DATE: 2000-03-06
PRIOR FILING DATE: 1999-12-08
NUMBER: OF SEQ ID NOS: 482
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                            Sequence 44967, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL.LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT PAPLICATION NUMBER: US 2002-203269
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 44967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 FVNVHDFNNFDEAIDYIKYLHTHPNAYLD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 IIDASKFSSLRELASYVKAVANDPVAYAE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 284, Application US/11197712
Publication No. US20060130160A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-449-902-44967
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Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE REPERENCE:
TITLE OF INVENTION:
FILE REPERENCE:
TOTO-15799US2
CURRENT FILING DATE:
CURRENT FILING DATE:
S04-09-30
NUMBER OF SQ IN DNOS: 40252
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:::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| ::::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 KRGVVSFVASNANAPMRNAFYDAL----NSIEPVTGGGSVKNTLGYNVKNKSFFLSQYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 323;
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Best Local Similarity 25.8%; Pred. No. 0.00017;
Matches 51; Conservative 34; Mismatches 78
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
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220 PKKRPCKCSRGGSDTVYH 237
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205 PKKRPCKCSRGGSDTVYH 222
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US-10-953-349-5127
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LENGTH: 338
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US-11-293-697-4748
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                                                                                                                                                          APPLICANT:
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250 RKRLAPLVYVQSYCDPPSDRDSYVRELMTYIEVDSYGECLRNKOLPQQLKNPASMDADGF 309
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                                                                                                                                                                                                                                               78 ARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKABSVN 137
                                                                                                                                                                                                                                                                                      135 ETGRIGQCGADACFFT-INRTYLHHHMTKAFLFYGTDFNIDSLPLP----RKAHHDWAVF 189
                                                                                                                                                                                                                                                                                                                                      138 DTTSP---YKLKDNSLYTLKKPSHQF-KENHPNLCAVVNDESDPLKR------- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 - EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNP--KEFVNVHD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 ANAPMRNAFYDALNSIEPV----TGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSQGY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 SNCGARNFRLQALEMLESLDVKIDSYGSCHRNHDG--KVDKVETLKRYKFSLAFENSNEE 287
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Sequence 52598, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TILES OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-AO20571-US

FURRENT FILING DATE: 2003-62-29

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR APPLICATION NUMBER: UP 2002-30369

PRIOR PLING DATE: 2002-105-30

PRIOR FILING DATE: 2002-105-30

PRIOR PLING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                          -----NEFSDLVPSNPLGS
                                                                                                                                                                                                                                                                                                                                                                                                                              181 ----GVVSFVASNANAPPRINAFY--DALINSIEPVTGGGSVKN-TLGYNVKNKS----
                                                                                                              Gaps
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                                                                                                              62;
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                                                                  Length 406;
                                                              Query Match 5.7%; Score 137; DB 7; Length 406
Best Local Similarity 24.5%; Pred. No. 0.0021;
Matches 80; Conservative 43; Mismatches 142; Indels
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                                                                                                                                                          35 GDEEIKEFKKSVLYPIFSQRYTIALHQNP---
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US-10-449-902-52598
; LOCATION: -31..-1
US-11-197-712-284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 PSHQPKENHPNLCAVVNDESDPLK-----RGVVSFVASNANAPMRNAFYDALNSIEP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 VTGGGSVKNTLGYNVKNKSEFLSQYKFN-----LCFENSQGYGYVTEKILDAYFSHT 259
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                                                                                                                                                           APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Daniel J.
APPLICANT: Sidney, John
APPLICANT: Sidney, John
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REFERENCE: EPI-103X
CURRENT PILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR APPLICATION NUMBER: 1161
SOFTWARE: Patentin version 3.2
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                                                                                                          The United States of America as Represented by the Secretary of the Navy Sette, Alessandro
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Publication No. US20060105376A1
GENERAL INPORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION WUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
Sequence 9, Application US/10537642
Publication No. US20060165719A1
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us-10-764-212-16.rapbn

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446 E----ENEKRNFNYYDTCKNIWNYQICKDDNNLLINNWEKTFFFFSNVNNWRYDECNNWN 500
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                                                                                                                                                                                                                                                                                                         620 NPIMMNINND------QINNLSIPNNKNEDNNEINHDD--SNDDDSNSSHITLM 665
                                                                                                                                                                  515 NDIS-----INKENNIFINMA---HILMHLDNHSYIQNNL-YKNHMNVNTNILYN 619
                                                                                                                                                                                                                                                           DIIYHKSSISEMWECDLDEPLASIDDLRV----NYDDLRVNYDDLRVNYDD-----LRVN 392
:|| |:
-------CNNFNKNINNNI 574
                                                                                                            282 HDFNNFDEAIDYIKYLHTHPNAYLDMLYENPLNALDGKAYFYQDLSFKKILAFFKTILEN 341
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APPLICANT: Epimmune, Inc.
APPLICANT: Epimmune, Inc.
APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Carucci, Denise L.
APPLICANT: Carucci, Daniel J.
APPLICANT: Southwood, Scott
APPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REFERENCE: EPI-103X
                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 KSDKNKNYPALNPKYQN-HQNHNINNIQNNLNEQIKEKNDQQNHNIKEIKN 716
                                                                                                                                                                                                                                                                                                                                                                                                             393 YDDLRVNYDDLRVNYERLLQNASPLLELSQNTSFKIYRKAYQ-----KPIKN 439
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CURRENT FILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: PATENTIN VERSION 3.2
                              536 LNVNNPTSSYNPPNINNMDSNIYNHTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10537642
Publication No. US20060165719A1
GENERAL INFORMATION:
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; ORGANISM: Plasmodium falciparum
US-10-537-642-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 KNKSEFLSQYKF-NLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 LRMPLYYDRLHHKAESVNDTT----SPYKLKDNSL-YTLKKPSH--QFK--ENHPNLCAV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PL----KRGVVSFVASN-ANAPMRNAFYDALNSIEP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 VIGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGYVTEKI----LDAYFSHTIPIY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 WG-SPSVAKDFNPKE-FVNVHDFNNFDEAIDYIKYLHTHPNAYLDMLYENPLNALDGKAY 321
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APPLICANT: Epimmune, Inc.
APPLICANT: Epimmune, Inc.
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Daniel J.
APPLICANT: Carucci, Daniel J.
APPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REPRENCE: EPI-103X
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
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                                                                                                                                                                                                                                                                                                     5.1%; Score 122; DB 7; Length 336; 25.1%; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                              98; Indels
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                                                                                                                                                                                                                                                                                                                                                                              41; Mismatches
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PRIOR APPLICATION NUMBER: US 60/431,494

PRIOR FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1161

SOFTWARE: Patentin version 3.2

SEQ ID NO 10

LENGTH: 3029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                              68; Conservative
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   NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Matches 75; Conserv
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Best Local Similarity
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                                                                         SEQ ID NO 4748
LENGTH: 336
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                                                                                                                                                                                                                                                                                Sequence 48384, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
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US-10-449-902-48384
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LENGTH: 615
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                                                                                                                          915 INKODYLHTDIVKNIDCVISPYKDPNIIMDRIN-DDNNINMDNLLFTYNEQWNNHHNNKK 973
680 NCNNYEKYINNMSFINNKESSNINKDDVYNGNMDNHNHHVNNNNTLCNTSLSDLCSNNSS 739
                                  243 GYGYVTEKILDAYFSHTIPIYWGSPSVAKD-----FNPKEFVNVHDFNNFDEAIDYIK 295
                                                      740 ESKKQEAVCLNKNDTHDI ----IKAVSNNMKRPSLYMNPINNNNNNNDDTSNNVO 794
                                                                                                    YLHTHPNAYL-----DMLYENPLNALDGKAYFYQDLS---FKKILAFFKTILENDTIYH 346
                                                                                                                                                                                                            855 KUVUBIMYSKEITNMNNINRSSDEYITNNNMDNDNNIMNYTLYPWKENKPKNVDMLNIYK 914
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APPLICANT: The United States of America as Represented by the APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Carucci, Daniel.J.
APPLICANT: Carucci, Daniel.J.
APPLICANT: Southwood, Scott
TITLB OF INVENTION: PLASMODIUM FALCIPARUM ANTICENS AND METHODS OF USE TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTICENS AND METHODS OF USE TITLE OF INVENTION: POS-06-06
THE REFERENCE: BPI-103X
CURRENT APPLICATION NUMBER: US 60/431,494
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SEQ ID NO 3
LENGTH: 2404
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                                                                                                                                                                                                                                                                                                                                           974 WNVFNNSIILEKNEKITNSKKKKNYKIHQR 1003
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Publication No. US20060165719A1
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ORGANISM: Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 CFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNV---HDFNNFDEAIDY 293
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-02-303870
PRIOR FILING DATE: 2002-02-303870
PRIOR FILING DATE: 2002-02-30
                                                                      515 VYNFLLKLLQRYEYSNILKSIRNSDLLNFFNSSİIQNLINFLCQKISQDVFIIEYD-DMP
                                                                                                                                                     362 LASIDDLRVNYDD-LRVNYD-----DLRVNYDDLRV------NYDDLRVNYDDLR
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4.6%; Score 109; DB 6; Length 615;
Best Local Similarity 19.8%; Pred. No. 0.75;
Matches 92; Conservative 73; Mismatches 174; Indels 126;
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SEQ ID NO 8
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APPLICANT: Carucci, Daniel J.
APPLICANT: Carucci, Daniel J.
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REFERENCE: EPI-103X
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.5%; Score 107; DB 6; Length 2024;
20.2%; Pred. No. 6.4;
tive 74; Mismatches 200; Indels 116;
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APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
508 RSGDVKSCKVARKTADAQPKELAKELKPLLTSLQSSSQSYQIWPK 552
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PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: Patentin version 3.2
LENGTH: 2024
                                                                                         Sequence 21, Application US/10537642
Publication No. US20060165719A1
GENERAL INFORMATION:
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ORGANISM: Plasmodium falciparum
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1132 LLDHSDDSS 1140
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Matches 99; Conserva
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RESULT 14 US-10-537-642-8

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                                                                                               APPLICANT: Epimmune, Inc.
APPLICANT: Epimmune, Inc.
APPLICANT: The United States of America as Represented by the
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Secrete, Jensel J.
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REFERENCE: EPI-103,
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
PRIOR PAPLICATION NUMBER: US 60/431,494
PRIOR PAPLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: Patentin version 3.2
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4.4%; Score 106; DB 6; Length 954;
Best Local Similarity 18.9%; Pred. No. 2.5;
Matches 95; Conservative 75; Mismatches 170; Indels 162;
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Publication No. US20060165719A1
GENERAL INFORMATION:
Sequence 8, Application US/10537642
Publication No. US20060165719A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Plasmodium falciparum
US-10-537-642-8
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               APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Doolan, Denise L.
APPLICANT: Carucci, Daniel J.
APPLICANT: Sidney, John
APPLICANT: Sidney, John
TITLE OF INVERTION PLASWODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
TITLE OF INVERTION NUMBER: US/10/537,642
CURRENT APPLICATION NUMBER: US 60/431,494
FILE REPERICATION NUMBER: US 60/431,494
PRIOR PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: Patentin version 3.2
SSC ID NO 27
LENGTH: 1464
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-537-642-27
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Best Local Similarity 20.0%; Pred. No. 4.8;
Matches 87; Conservative 60; Mismatches 159; Indels 128; Gaps
Secretary of the Navy
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Search completed: August 11, 2006, 19:54:05 Job time : 18.9493 secs

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                   Copyright
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 protein search, using sw model OM protein

August 11, 2006, 19:30:38 ; Search time 116.066 Seconds Run on:

(without alignments)
1733.289 Million cell updates/sec

US-10-764-212-18

2362 1 MFQPLLDAFIESASIKKMPL.....YHKSLPLLRAIRRWVKKLGL 440 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2589679 Total number of hits satisfying chosen parameters:

2589679 seqs, 457216429 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A\_Geneseq\_8:\* Database

geneseq1990s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\*geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\* geneseqp2005s:\*

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## SUMMARIES

		de					
Result No.	Score	Query	Length	DB	ID	Description	
	2362	100.0	440	6	ABB70147	Aeb70147 Helicobac	
7	2347	99.4	440	'n	ABG30883	Abg30883 H. pylori	
٣	2007.5	85.0	485	œ	ADJ77814		
4	2007.5	85.0	485	œ	ADJ27349	σ	
S	2007.5	85.0	485	σ	AEB70135	Aeb70135 Helicobac	
9	2006.5	84.9	454	'n	ABG30887	Abg30887 H. pylori	
7	1999	84.6	486	α	ADJ77810	Adj77810 Helicobac	
ω	1999	84.6	486	æ	ADJ27345	Adj27345 Alpha-1,3	
σ	1999	84.6	486	σ	AEB70131	Aeb70131 Helicobac	
10	1984.5	84.0	485	Ŋ	ABG30882	Abg30882 H. pylori	
11	1982.5	.83.9	476	ഹ	ABG3 0884	Ħ	
12	1978	83.7	464	7	AAW86008		
13	1970.5	83.4	432	œ	ADJ77812	Adj77812 Helicobac	
14	1970.5	83.4	432	00	ADJ27347	Adj27347 Alpha-1,3	
15	1970.5	83.4	432	σ	AEB70133	Aeb70133 Helicobac	
16	1970	83.4	501	Ŋ	ABG30881	Ξ.	
17	1960.5	83.0	479	Ŋ	ABG30886	Ħ.	
18	1879.5	79.6	425	œ	ADJ77820	Hel	
19	1879.5	79.6	425	ω	ADJ27355	Adj27355 Alpha-1,3	
20	1879.5	79.6	425	σ	AEB70141		
21	1869	79.1	424	Ŋ	ABG30885	Abg30885 H. pylori	
22	1861	78.8	446	σ	AEB70145	5 He	
23	1842.5	78.0	418	Ŋ	ABU52257	Abu52257 Helicobac	

5	Ċ	Aeb70195 H. pylori	æ	Adj77816 Helicobac	Adj27351 Alpha-1,3	Aeb70137 Helicobac	Η.	Aeb70204 H. pylori	Aeb70203 H. pylori	Aeb70193 H. pylori	Aeb70201 H. pylori	Aeb70202 H. pylori	Aeb70206 Helicobac	Aeb70205 H. pylori	Aeb70211 Helicobac	Aeb70154 H. pylori	Aeb70212 Helicobac	Abu51720 Helicobac	Abu51151 Helicobac	Abu51509 Helicobac	Abu51153 Helicobac	The Part of the Contract of
2010101	AEB/019/	AEB70195	AEB70149	ADJ77816	ADJ27351	AEB70137	AEB70199	AEB70204	AEB70203	AEB70193	AEB70201	AEB70202	AEB70206	AEB70205	AEB70211	AEB70154	AEB70212	ABU51720	ABU51151	ABU51509	ABU51153	
1	3//	391 9	456 9	277 8	277 8	277 9	256 9	246 9	246 9	231 9	245 9	247 9	250 9	247 9	559 9	227 9	545 9	146 5	169 5	130 5	124 5	
	7.7	75.6	73.6	50.3	50.3	50.3	48.5	48.5	48.3	47.0	46.9	46.4	45.6	44.2	43.3	42.0	37.0	25.0	24.0	22.5	21.0	
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;	77	52	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	

#### ALIGNMENTS

Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 18. Bezila DJ; Fucosyltransferase; protein production; enzyme Simala-Grant J, Taylor D, Johnson KF, /note= "Encoded by TTT" Location/Qualifiers AEB70147 standard; protein; 440 AA. Helicobacter pylori; strain 802. (NEOS-) NEOSE TECHNOLOGIES INC. (UYAL-) UNIV ALBERTA. 22-JAN-2004; 2004US-00764212. 22-JAN-2004; 2004US-00764212. (first entry) WPI; 2005-521417/53. N-PSDB; AEB70146. Misc-difference 112 US2005164338-A1. 06-0CT-2005 28-JUL-2005. AEB70147; 

The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucosyltransferase polynucleotides and acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein. New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids. Claim 1; SEQ ID NO 18; 97pp; English.

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421 YHKSLPLLRAIRRWVKKLGL 440
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                                                                                                          NEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYLRMP
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                                                                                                                                                                                       SFVASNPNAPKRNAFYDALNSI EPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFENSQG
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
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                             Length 440;
                                                 Indels
                            100.0%; Score 2362; DB 9;
100.0%; Pred. No. 2.7e-208;
ive 0; Mismatches 0;
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                                      Best Local Similarity 100.
Matches 440; Conservative
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The invention relates a purified transmembrane segment-free alpha 1,3-
the invention relates a purified transmembrane segment-free alpha 1,3-
the Complement of the sequence: X.1-X.2-
Leu-Arg-X.3-X.4-Tyr, where X.1, X.2 and X.4 is Asp or Asn; and X.3 is
Leu-Arg-X.3-X.4-Tyr, where X.1, X.2 and X.4 is Asp or Asn; and X.3 is
Leu-Arg-X.3-X.4-Tyr, where X.1, X.2 and X.4 is Asp or Asn; and X.3 is
Leu-Arg-X.3-X.4-Tyr, where X.1, X.2 and X.4 is Asp or Asn; and X.3 is
Leu-Arg-X.3-X.4-Tyr, where X.1, X.2 and X.4 is Asp or Asn; and X.3 is
Cording the complement or fragment), a vector containing the mucleic acid or vector, an antibody which
comprising a host cell containing mucleic acid or vector, an antibody which
comprising a host cell modified with the mucleic acid or its
comprising the produced oligosaccharides, such as Lex, Ley or SLex, by
contacting the produced oligosaccharides, such as Lex, Ley or SLex, by
contacting the bots cell with a substrate, to produce oligosaccharides
and purifying the obtained oligosaccharides. The mucleic acid is useful
contacting the obtained oligosaccharides. The mucleic acid is useful
as a probe for detecting the mucleic acid, by contacting a sample with a
cucleic acid probe that hybridises to alphal.3-fucosyltransferase
contacting the mucleic acid, and actenting the mucleic acid, by contacting a sample with a
cucleic acid probe that hybridises to alphal.3-fucosyltransferase-fusion prodein, by growing the host cell containing a
cucleic acid probe that hybridises to alphal.3-fucosyltransferase-fusion prodein, by growing the host cell containing a
cucro reperiod under acidish polymerase chain reaction (PCR)
cucosyltransferase-fusion prodein, by growing the host cell containing
cucleic admining a sample. The protein in a sample is indicative of infection by Helicobacter pylori or the protein
confidence and monitoring disease, and for inhibiting abnormal applal.3-
cucosyltransferase gene product activity. The nucleic acid all seconds and polyment of a seasys to detect
confidence and conditi
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Claim 6; Fig 6; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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237

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241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFNDFAIDHVRYLHTH 300
                                                                                                                                                                                                 358 VSIDDLRADYNNIRADYNNIRADYNNIRADYNNIRADYD------ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contexting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucosy residue from a donor substrate to the acceptor substrate to the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and acceptor substrate on glycoprotein.
178 GFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN
                                                            SOGYGYVTEKIIDAYFSHTIPIYWGSPSVAKOFNPKSFVNVHDFKNFDEAIDYVRYLHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
fucosyl; fucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori; strain 1218 FutB.
                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ27349 standard; protein; 485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-1,3/4-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEOS-) NEOSE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 3; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2003; 2003WO-US023155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson KF, Bezila DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-132958/13.
N-PSDB; ADJ27348.
                                                                                                                                                                                                                                                                                                            KKLGL 440
                                                                                                                                                                                                                                                                                                                                         481 KKLGL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004009793-A2
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                                                             238
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                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Futh and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of altrosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to sumamialian expression systems. This polypeptide sequence is an H. pylori strain 1218 FutB protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONPNEPSDLVFGSPIGSARKILSYQNAKRVFYTGENESPNFNLFDYAIGFDELDFRDKYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPQPLLDAFIESASIKKM-PLSYPPLKIAVANWWGG--AEEFKKSAMYFILSQRYTITLH
                                                                                                                                                                                                                  FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; Score 2007.5; DB 8; Length 485; 78.1%; Pred. No. 1.3e-175; index 34; Mismatches 27; Indels 45;
                                                                                                                                                                                    Helicobacter pylori strain 1218 FutB protein SeqID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; SEQ ID NO 6; 72pp; English.
                                                                                           ADJ77814 standard; protein; 485 AA
                  440
                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEOS-) NEOSE TECHNOLOGIES INC
421 YHKSLPLLRAIRRWVKALGL
                                                                                                                                                                                                                                                                                                                                                        23-JUL-2003; 2003WO-US023057.
                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 78.1%;
Matches 379; Conservative 3
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KF, Bezila DJ;
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                                                                                                                                                                                                                                                              Helicobacter pylori.
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                                                                                                                                                       06-MAY-2004
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                                                                                                                        ADJ77814;
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                                                                    QNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYL 117
                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated fucosyltransferase polynucleotides and polypeptides, useful
                                            SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLHTH
                                                                                                                                                                                                                                                        RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR
                                                                                                                 RMPLYYDRIHHKAESVNDTTSPYKLKDDSLYALKKSHHFKENHPNLCAVVNNBSDPLKR
                                                                                                                                          GFAS FVASNPNAPKRNAFYDALNS I EPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN
                                                                                                                                                                            SQGYGYVTEKIIDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNPDEAIDYVRYLHTH
                                                                                                                                                                                                             PNAYLDMLYENPLATLDGKAYFYQDLSFKKILDPFKTILENDTIYHNNPFVFYRDLNEPL
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                                  MPQPLLDAFIESASIKKM-PLSYPPLKIAVANWWGG--AEBFKKSAMYFILSQRYTITLH
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO:
                 45;
Length 485;
                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bezila DJ;
DB 8;
                                                                                                                                                                                                                                                VSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYD-
; Score 2007.5; DB 8
; Pred. No. 1.3e-175;
34; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pucosyltransferase; protein production; enzyme
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                                                                                                                                                                                                                                                                                                                                                                                 AEB70135 standard; protein; 485
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85.0%;
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                 Matches 379; Conservative
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N-PSDB; AEB70134.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     KKLGL 485
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AEB70135
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                                                            The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                    ONFNEPSDLVFGSPIGSARKILSYQNAKRVFYTGENESPNFNLFDYAIGFDELDFRDRYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNAYLDMLYENPLATLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bnzyme, fucT, alphal,3 fucosyltransferase; oligosaccharide, Lex; Ley;
sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDPNPKSFVNVHDFKNFDEAIDYVRYLHTH
                                                                                                                                                                                                                                                                                                                 ONPNEPSDLVFGSP1GAARK11LSYQNTKRVFYAGENEVPNFNLFDYA1GFDELDLRDRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                 RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFQPLLDAPIESASIKKM-PLSYPPLKIAVANWWGG--AEEFKKSAMYFILSQRYTITLH
                                                                                                                                                                                                                                                                 Gaps
for synthesizing oligosaccharides, glycoproteins, or glycolipids
                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                DB 9; Length 485;
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                                                                                                                                                                                                                            85.0%; Score 2007.5; DB 9; Length
78.1%; Pred. No. 1.3e-175;
ive 34; Mismatches 27; Indels
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                             Example 1; SEQ ID NO 6; 97pp; English
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.18
Matches 379; Conservative
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(first entry)
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                                                                                                                                                                                                 Sequence 485 AA;
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21-OCT-2002
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84.6%; Score 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
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(throsyltransferase polypebtide, having a repeat of the sequence: X.1-X.2-
[Leu-Arg-X.3.4-Tyr, where X.1, X.2 and X.4 is Asp or Ann; and X.3 is
[Leu-Arg-X.3.4-Tyr, where X.1, X.2 and X.4 is Asp or Ann; and X.3 is
[Leu-Arg-X.3.4-Tyr, where X.1, X.2 and X.4 is Asp or Ann; and X.3 is
[Inc.yulor Ala. Also included are the nucleic acid encoding the protein
[C cid.d. a host cell containing uncleic acid or vector, an antibody which
selectively binds to the protein and a gene expression system for
selectively binds to the protein and a gene expression system for
producing transmembrane segment-free alpha! 3- fucosyltransferase,
comprising a host cell modified with the nucleic acid or its
comparising the protein with a substrate such as Lex. Ley or SLex, by
contacting the protein with a substrate, to produce oligosaccharides
contacting the protein with a substrate, to produce oligosaccharides
contacting the bots cell with a substrate, to produce oligosaccharides
contacting the bots cell with a substrate, to produce oligosaccharides
a probe for detecting the mucleic acid, by contacting a sample with a
nucleic acid probe that hybridises to alpha!, 3-fucosyltransferase
contacting the obtained oligosaccharides. The nucleic acid is useful
as a probe for detecting hybridises to alpha!, 3-fucosyltransferase
contacting the nucleic acid using polymerase chain reaction (PCR). The
nost cell is useful for producing a transmembrane segment-free alpha!, 3-
contacting the protein my protein. The antibody is useful
cor peptide under conditions which allow expression and secretion of the
cor peptide under conditions which allow expression and secretion of the
cusoyltransferase gene product activity. The nucleic acid is useful
cor detecting the protein in a sample. The presence of the protein in the
amplituant cells. The antibody is also useful for diagnosing disorders
and monitoring disease, and for inhibiting abnormal alpha!, 3-
cucosyltransferase gene regulation. O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONPNEPSDLVFGSPIGAARKILSYONTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHPKEKHPHLCAVVNDESDPLKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFQPLLDAFIESADIEKWASKSPPPLKIAVANWWGDEIKEFKKSTLYFILSQHYTITLH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                    Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%; Score 2006.5; DB 5; Length 454; 82.6%; Pred. No. 1.5e-175; Live 35; Mismatches 27; Indels 17;
                                                                                                                                                                                                                                 Example 3; Fig 6; 37pp; English
                               07-DEC-2000; 2000US-00733524.
                                                             98US-00092315.
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Best Local Similarity
Matches 375; Conservat
                                                                                           (UYAL-) UNIV ALBERTA
                                                                                                                                                      WPI; 2002-582480/62.
                                                                                                                         Ge 2;
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                                                             05-JUN-1998;
06-JUN-2002
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403
                                                                                                                                     241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKOFNPKSFVNVHDFNNFDEAIDYVRYLHTH 300
                                                                                                                                                                                                                                                                                                              This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Fuths and Futs) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moleties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, absterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 1182 FutB protein sequence of the invention.
181 GFASFVASNANAPMRNAFYDALNSIEPVTGGGAVKNTLGYKVGNKSEFLSQYKFNLCFEN 240
                                                                                                                                                                                                                                                                PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNEPL 357
                                                                                           SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYD-------RLLQNRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Futh, Futh, Puth alpha 1-3/4 fucosyltransferase, glycoprotein; glycolipid, fucose, N-acetylglucosamine, glycoconjugate, enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori strain 1182 FutB protein SeqID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 PLLELSQNTTFKIYHKAYHKSLPLLRAIRRWVKK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 PLLELSQNTSFKIYRKIYQKSLPLLRVIRRWVKK 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ77810 standard; protein; 486 AA.
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US2005164338-A1
                                                                                                                             Sequence 486 AA;
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Matches
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                                                                                                                                                                                                                                                                                       NNLRADYNNLRADYNNLRADYDRLLQNRSPLLELSQNTTFKIYHKAYHKSLPLLRAIRRW 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and
                                                                                                           ONPNEPSDLVPGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYL
                                                                                                    RMPLYYDRLHHKAESVNDTTAPYKI KPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR
                                                                                                                                      GFAS FVASINPNA PKRNA FYDALNS I EPVTGGGSVKNTLGYKVGNKNE FLSQYKFNLCFEN
                                                                                                                                                                           SQGYGYVTEKI I DAYFSHTI PI YWGSPSVAKDPNPKSPVNVHDPKNFDEAI DYVRYLHTH
                                                                                                                                                                                                                                                   VSI-----DDLRADYNNLRADY
                           1 MFQPLLDAFIESASIKKM-PLSYPPLKIAVANWWGG--AEEFKKSAMYFILSQRYTITLH
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
          46;
          Indels
77.6%; Pred. No. 8.2e-175; tive 35; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori; strain 1182 FutB
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                                                                                                                                                                                                                                                                                                                                                                                          ADJ27345 standard; protein; 486
                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-1,3/4-fucosyltransferase.
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08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
Best Local Similarity 77.6% Matches 377; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KF, Bezila DJ
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                                                                                                                                                                                                                                                                                                                                       #81 IKKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fucosyl; fucose.
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                                                                             This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoportein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN
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                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                   Length 486;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                               84.6%; Score 1999; DB 8; 77.6%; Pred. No. 8.2e-175; tive 35; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fucosyltransferase; protein production; enzyme
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acceptor substrate on glycoprotein.
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                                           Claim 1; Fig 1; 84pp; English
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.6
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                                                                                                                                                                                                                                                                                                                                                                                              ONPNEPSDLVPGSPIGAARKILSYONTKRVFYAGENEVPNFNLPDYAIGFDELDLRDRYL 117
                                                                                                                                                                                                                                                                                                                                                                                                                           RMPLYYDRLHHKAESVNDTTAPYXIKPDSLYTLKKPSHHPKEKHPHLCAVVNDESDPLKR 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQCYCYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLHTH 300
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                                                                                                                                           New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
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361 ISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY
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                                                                                                                                                                                                                                                                                                  84.6%; Score 1999; DB 9; Length 486; 77.6%; Pred. No. 8.2e-175; Live 35; Mismatches 28; Indels 40
                                                                                          Johnson KF, Bezila DJ;
                                                                                                                                                                         Example 1; SEQ ID NO 2; 97pp; English.
                                                           NEOS-) NEOSE TECHNOLOGIES INC
                                        22-JAN-2004; 2004US-00764212.
                                                                                          Simala-Grant J, Taylor D,
                                                                                                                                                                                                                                                                                                                       Matches 377; Conservative
                                                                     (UYAL-) UNIV ALBERTA
                                                                                                              WPI; 2005-521417/53.
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                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                         N-PSDB; AEB70130.
                                                                                                                                                                                                                                                                                Sequence 486 AA;
28-JUL-2005
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The invention relates a purified transmembrane segment-free alpha 1,3-
fucusyltransferase polypeptide, having a repeat of the sequence: X1-X2-
leu-Argy-X3-X4-Ty, where X1, X2 and X4 is Aap or Asn; and X-3 is
leu-Argy-X3-X4-Ty, where X1, X2 and X4 is Aap or Asn; and X-3 is
cleid, a host call containing nucleic acid or vector. an antibody which
acid, a host call containing nucleic acid or vector, an antibody which
comprising a host cell modified with the nucleic acid or its
comprising a host cell modified with the nucleic acid or its
comprising a host cell modified with the nucleic acid or its
comprising the protein with a substrate such as LackNc-R and GDP-fucose,
contacting the protein with a substrate, to produce oligopaccharides
contacting the protein with a substrate, to produce oligopaccharides
contacting the protein with a substrate, to produce oligopaccharides
and purifying the obtained oligosaccharides. The nucleic acid is useful
contacting the botained oligosaccharides. The nucleic acid is useful
as a probe for detecting the nucleic acid, by contacting a sample with a
nucleic acid probe that hybridises to alpha1,3-fucosyltransferase
contacting the nucleic acid using polymerase chain reaction (PCR). The
polymucleotide, and detecting hybridisation of the probe; or by
contacting the nucleic acid using polymerase chain reaction (PCR). The
host cell is useful for producing a transmembrane segment-free alpha1,3-
corposyltransferase-fusion protein, by growing the host cell containing a
cuctor operably linked to a polymucleotide encoding a desired polypeptide
cor peptide under conditions which allow expression and secretion of the
cuspile indicative of infection by Helicobacter pylori or the presence
cor memoritoring disease, and for inhibiting abnormal alpha1,3-
cof malignant cells rhe antibody is also useful for diagnosing disease, and for inhibiting abnormal alpha1,3-
cof maniforang case gene product activity. The nucleic acid is suseful as
fucosyltransferase gene product activity. The nucleic acid is an equ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian tunmours. The present sequence represents an H. pylori alphal,3 fucosyltransferase encdoed by the fucT gene. (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                                                                                     Bnzyme; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley;
sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
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                                                                                                                                                                                                                       H. pylori alphal, 3 fucosyltransferase #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori; strain 1182
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                                                                                                                                         (first entry)
                                                                                        (revised)
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                                                                                   29-AUG-2003
21-OCT-2002
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ABG30882;
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4

Gaps

47;

ABG30882 standard; protein; 485 AA.

RESULT 10 ABG30882

us-10-764-212-18.rag

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240
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                                                                  RMPLYYDRIAHKAESVNDTTSPYKLKPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKR
                                                                                                                                     241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLHTH
                                                                                                                                                                      ; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley;
Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                         RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR
                                                                                                  SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDPNPKSPVNVHDFKNPDEAIDYVRYLHTH
                                                                                                                                                             PNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNEPL
                                                                                                                                                                                                        GPASFVASINPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCPEN
1 MFQPLLDAYIESASIEKITSKSPPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLH
                                                                                                                                                                                                                                                                                                                                                                                      H. pylori alphal, 3 fucosyltransferase #4.
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(first entry)
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21-OCT-2002
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Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.

98US-00092315

15-JUN-1998;

(UYAL-) UNIV ALBERTA

Ge Z;

Taylor DE,

VPI; 2002-582480/62

07-DEC-2000; 2000US-00733524

06-JUN-2002

Example 3; Fig 6; 37pp; English

C The invention relates a puritied transmembrane segment-tree alpha 1,3-c tucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2 c tucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2 c tucu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is 1 c teu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is 1 c 1 c 1 c Arg in the mucleic acid or vector, an antibody which selectively binds to the protein and agene expression system for containing the tree laplat, 3-fucosyltransferase, comprising a host cell modified with the nucleic acid or its contacting the protein with a substrate such as LackNac-R and GDP-fucose, contacting the protein with a substrate such as LackNac-R and GDP-fucose, contacting the protein with a substrate, to produce oligosaccharides, or by culturing the cell, contacting the protein with a substrate, to produce oligosaccharides, or by culturing the protein with a substrate, to produce oligosaccharides, or by culturing the bost cell with a substrate, to produce oligosaccharides, and purifying the produced oligosaccharides. The nucleic acid is useful as a probe for detecting the host cald using polymerse chain reaction (PCR). The polymelectide, and detecting phyridisation of the probe; or by contacting the nucleic acid using polymerse chain reaction (PCR). The contact operably linked to a polymerse chain reaction (PCR). The cost cell is useful for producing a transmembrane segment free alphal, 3-c fucosyltransferase-fusion protein, by growing the host cell containing a cettor operably linked to a polymerse chain reaction (PCR). The cost conditions which allow expression and secretion of the protein or cell are angele is indicative of infection by elections. The antibody is also useful for diagnosing disease, and for inhibiting abnormal alphal, 3-c fucosyltransferase gene product activity. The nucleic acid is an angle is indicative of infection or cell are useful in the development of assays to detect the protein or cell are negalat 176 236 296 356 -----DDLRADYNNLRADYNNLRADY 381 9 1 MFQPLLDAFIESASIEKAYVSKSPPPPLKIAVANWWGDEBIKEFKKSVLYFILSQRYAITL 241 NSQGYGYVTEKILDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEALDYIKYLHT NSQGYGYVTEKI I DAYPSHTI PI YWGS PSVAKDFNPKS FVNVHDPKNFDEAI DYVRYLHT HPNAYLDMLYENPLNTLDGKAYFYQDLSPKKILDFFKTILENDTIYHNNPFVFYRDLNEP |:|| 361 LISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY RGFAS FVASNPNAPKRNAPYDALNS I EPVTGGGS VKNTLGYKVGNKNEFLSQYKFNLCFE transmembrane segment-free alpha 1,3-117 LRMPLYYDRIHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLK NNLRADYNNLRADYDRLLQNRSPLLELSQNTTFKIYHKAYHKSLPLLRAIRRWVKK 437 1 MFQPLLDAFIESASIKKMPLSY--PPLKIAVANWWGGAE--EFKKSAMYFILSQRYTITL Gaps 39; Length 476; 33; Indels 83.9%; Score 1982.5; DB 5; 78.6%; Pred. No. 2.6e-173; Live 30; Mismatches 33; I. Best Local Similarity 78.6% Matches 374; Conservative 357 LVSI-----standardise OS field) Sequence 476 AA; 382 297 177 Query Match g 셤 셤 8 셤 ઠ ठ ò ઠે 8 셤 ò 셤 ઠ g

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and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated alpha-1-3-fucosyltransferase gene - obtained from Helicobacter pylori, used to develop products for the diagnosis treatment of intestinal mucosal diseases, e.g. tumours.
                                                                                                      Alpha-1,3-fucosyltransferase; fucT gene; Lewis X; Lewis Y; sialyl Lewis X; tumour associated antigen; cancer; infection; mucosal disease; diagnosis; fucosylated oligosaccharide.
                                                                                     Helicobacter pylori alpha-1,3-fucosyltransferase
                                                                                                                                                                         96. .99
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                 /note= "Asn is N-glycosylated" 332 ...334 /note= "Asn is N-glycosylated" 341 ...343 /note= "Asn is N-glycosylated" /note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
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378. 384
note= "peptide repeat"
385. 391
note= "peptide repeat"
322. 398
/note= "peptide repeat"
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/note= "peptide repeat"
413. .419
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/note= "peptide repeat"
371. .377
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                                                                                                                                             Helicobacter pylori; strain NCTC 11639
                                                                                                                                                                 Location/Qualifiers
                   AAW86008 standard; protein; 464 AA.
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/ . . . 405
/note= "per
                                                                  (first entry)
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                                                         (revised)
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Modified-site
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                                                       17-OCT-2003
29-MAR-1999
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                                      AAW86008;
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RESULT 12
AAW86008
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This is the amino acid sequence of the novel alpha-1,3-fucosyltransferase of Helicobacter pylori NCTC 11639, as deduced from the newly isolated fucT gene (see AAV80321). The enzyme is characterised by 8 C-terminal heptad repeats and by the lack of a transmembrane domain. The absence of a transmembrane domain allows the enzyme to be readily

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released from recombinant host cells. The enzyme can be used in the production of fucosylated oligosaccharides such as Lewis X, Lewis Y and slalyl Lewis X, which are structurally similar to certain tumour associated antigens found in mammals. These glycoconjugates also have research and diagnosis utility in the development of assays to detect mammalian tumours. The enzyme can also be used to raise specific antibodies. Inhibition of abnormal fucT gene product activity can be used to the treatment of intestinal mucosal disease. (Updated on 17-oct-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                          RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GFASFVASIVPIAPIRINAFYDALINSIEPVTGGGSVRNTLGYNVGNKINEFLRQYKENLCFEN 240
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                                                                                                                                                                                                                                                             1 MFQPLLDAFIESASIKKM-PLSYPPLKIAVANWWGGAE--EFKKSAMYFILSQRYTITLH
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fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                         34; Indels 24; Gaps
                                                                                                                                                                                               Length 464;
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                                                                                                                                                                                              83.7%; Score 1978; DB 2;
80.6%; Pred. No. 6.6e-173;
ive 32; Mismatches 34;
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08-NOV-2002; 2002US-0424894P.
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Matches 374; Conservative
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                                                                                                                                                                   Sequence 464 AA;
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(NEOS-) NEOSE TECHNOLOGIES

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Sequence 432 AA;
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                                                                                                                                                                         This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Futh and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to Nacctylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expression systems. This polypeptide sequence is an H. pylori strain 1111 FutA protein sequence of the invention.
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                                                                                          New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
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82.5%; Pred. No. 2.9e-172;
ive 39; Mismatches 29;
                                                                                                                                                  Claim 16; SEQ ID NO 4; 72pp; English
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Best Local Similarity 82.5'
Matches 362; Conservative
                           Johnson KF, Bezila DJ
                                                   WPI; 2004-123401/12.
N-PSDB; ADJ77811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoptotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucosy residue from a donor substrate the acceptor substrate on the producing fucosylated glycoprotein. The method is useful for producing fucosylated glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                              Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate acceptor substrate on glycoprotein.
                                         alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase; fucosyl; fucose.
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82.5%; Pred. No. 2.9e-172;
ive 39; Mismatches 29;
                                                                                         Helicobacter pylori; strain 1111 FutA
           Alpha-1,3/4-fucosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2; 84pp; English
                                                                                                                                                                                                                      23-JUL-2002; 2002US-0398156P.
08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                    23-JUL-2003; 2003WO-US023155
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Matches 362; Conservative
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N-PSDB; ADJ27346.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
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                                                                                                                                                                                   Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 4.
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Best Local Similarity 82.5%; Pred. No. 2.9e-172;
Matches 362; Conservative 39; Mismatches 29; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bezila DJ;
                                                                                                                                                                                                                 Fucosyltransferase; protein production; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson KF,
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                                                                                                  AEB70133 standard; protein; 432 AA
                419 KAYHKSLPLLRAIRRWVKK 437
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UNIV ALBERTA.
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Title: Perfect score: Sequence:

US-10-764-212-18 2362 1 MPQPLLDAFIESASIKKMPL.....YHKSLPLLRAIRRWVKKLGL 440

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	Length	436	476	454	425	346	513	183	433	451	324	400	789	3973	405	393	525	631	1272	361	3394	810	414	605	608	689	689	365	402
di	Query	86.3	83.9	83.0	79.6	7.9	6.9	6.2	5.8	5.7	5.5	5.4	5.4	5.4	5.3	5.2	5.2	5.2	5.5	5.2	5.1	5.1	5.1	5.1	5.0	5.0	5.0	5.0	u
	Score	2039	1982.5	1960.5	1879.5	187	160.5	147.5	137.5	134.5	129.5	128.5	127.5	126.5	124.5	124	124	124	123.5	123	121.5	120.5	120	119.5	119	118.5	118.5	117.5	117
	Result No.	1	~	ო	4	2	9	7	œ	σ	10	11	12	13	14		16	17	18	19	20	21	22	53	24	52	56	27	28

SERA antigen/papai	type I restriction	hypothetical prote	type I restriction	hypothetical prote	hypothetical prote	hypothetical prote	alpha-(1,3)-fucosy	alpha (1,3) fucosy	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	major merozoite su
A71617	B75221	G71609	C64695	C82931	E71604	F82884	A45156	I39048	A84150	E70204	T18460	T18416	G71611	G71613	805603
7	~	~	~	~	~	~	0	8	~	~	~	~	~	~	0
1004	1104	2500	817	1084	2380	5005	359	364	624	1146	836	1338	2206	1346	1639
4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7
116.5	116	115.5	115	114.5	114	114	113.5	113.5	113.5	112.5	112	112	111.5	110.5	110.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

	RESULT 1
	G71862
	alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
	C;Species: Helicobacter pylori
	A;Variety: strain J99
	C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
	C;Accession: G71862
	R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
	; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; I
	Nature 397, 176-180, 1999
	A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
	A; Reference number: A71800; MUID:99120557; PMID:9923682
	A;Accession: G71862
	A;Status: preliminary
	A; Molecule type: DNA
	A;Residues: 1-436 <arn></arn>
	A;Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI00000036D2; GB:AE001528; GB:AE001439; NID:
	A;Experimental source: strain J99
	Query Match 86.3%; Score 2039; DB 2; Length 436;
	Matches 384; Conservative 25; Mismatches 23; Indels 12; Gaps 3;
	Oy 1 MPQPLLDAFIESASIKCMPLSYPPLKIAVANWWGGAEEFKKSAMYFILSQRYTITL 56
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ii	_;		
qq	Σ.	MFQPLLDAFIESTFIKK-KITFKSPPPPLKIAVANWWGGAEEFKKSTLIFTLSQKITTIL 59	ת
à	57 H	57 HONPIBESDLVFGSPIGAARKILSVQNTKRVFYAGENEVPNFNLFDVAIGFDELDLRDRY 116	116
qq	- 09	QNPNEPSDLVLGSPIGSARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFRDRY	119
ò	117 L	117 LRMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLK 176	921
DÞ	120 L	RMPLYYASLHYKAESVNDTTAPYKLKDNSLYALKKPSHHFKENHPNLCAVVNDESDPLK	641
ò	177 R	177 RGFASFVASNPNAPKRNAFYDALNSIBPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFE 236	36
qu	180 R	180 RGFASFVASNPNAPIRNAFYDALNSIBPVTGGGSVROTILGYNVKNKSBFLSOYKFNLCFE 239	239

	FVNVHDFKNFDEAIDYVRYLHT 296
	237 NSQGYGYVTEKIIDAYPSHTIPIYWGSPSVAKDFNEKSFVNVHDFKNFDEAIDYVRYLHT 296 
236 מפוא זו מטיפון אמנועי ביירוואם ביירוים או ביירוים או ביירוים או ביירוים או ביירוים או ביירוים ביירוים ביירוים ביירוים ביירוים ביירוים או ביירוים ב	237 240
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: C64567
R;Tomb, J.F; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, B.; Hayes, W.S.; Borcodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.h A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467; PMID:9252185
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                                 A;Molecule type: DNA
A;Residues: 1-454 <ARN>
A;Residues: 1-454 <ARN>
A;Cross-references: UNIPROT:Q9ZLI3; UNIPARC:UPI0000D3665; GB:AE001491; GB:AE001439; NLD:
A;Experimental source: strain J99
C;Genetics:
A;Gene: fucT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 NTQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVCDFRNFDEAIDYVRYLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVSI-------DDLRADYNNLRADYNNLRADYNNLRADYNNLRADYNNLRADYDRLLQNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFE
                                                                                                                                                                                                                                                                                                                                                                                              LRMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLK
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                                                                                                                                                                                                                                                                                                                                                         1 MFQPLLDAFIESASIKKMPLSYPPLKIAVANWW----GGAEEFKKSAMYFILSQRYTITL
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                         DB 2; Length 454;
                                                                                                                                                                                                                                                                                                34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fucosyltransferase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
                                                                                                                                                                                                                                   Query Match 83.0%; Score 1960.5; DB 2, Best Local Similarity 80.9%; Pred. No. 2.6e-129; Matches 368; Conservative 34; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLLELSQNTTFKIYHKAYHKSLPLLRAIRRWVKK 437
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      A;Status: preliminary
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                                                                                                                                                                      alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004
C;Accession: B71914
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; I ves, C.; Gibson, R; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Artie: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGPASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFE 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HONPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPNAYLDMLYENPLWTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNEP 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.9%; Score 1982.5; DB 2; Length 476; 78.6%; Pred. No. 8e-131; Live 30; Mismatches 33; Indels 39;
                                       436
413 YRKAYQKSLPLLRAIRRWVKKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 78.68
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: B71914
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; M. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-513 <STO>
A;Cross-references: UNIPROT:Q9FX97; UNIPARC:UPI00000BDB7; GB:AE005173; NID:g10120428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Ricketisia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97832
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
Since 293, 2093-2099, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 PDSLYTL-KKP-----SHHFKEKHPHLCAVVNDESDPLKRGF----ASFVASNPNAP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NDTIYHNNPFVFYRDLNEPLVS 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 FSWAEYDIMSPVQPKTERAIAAAFISNCGARNFRLQALEALMKTNIKIDSYGGCHRNRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 YKVGNKNEFLSQYKPNLCFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNP--KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 -KV-DKVEALKRYKFSLAFENTNEEDYVTEKFFQSLVAGSVPVVVGPPNI-EEFAPASDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 AAVHSSCRLCIFLATRVREQEEESPNFKKRPCKCSRGGSDTVYH-----VFVRERGRFEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 KRNAFYDALNSIEPVTG------GGSVKNTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVNVHDFKNFDEAIDYVRYLHTHPNAYLDML---YENPLNTLDGKAYFYQDLSFKKILD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Mismatches 107; Indels 115;
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6.2%; Score 147.5; DB 2; Length 183;
Best Local Similarity 28.6%; Pred. No. 0.0025;
Matches 44; Conservative 22; Mismatches 69; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 160.5; DB 2;
Pred. No. 0.0013;
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Best Local Similarity 22.1%;
Matches 78; Conservative 5:
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
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A;Gene: F14J22.8
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probable fucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96533
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y. Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae Ol39 are close A;Reference number: Z22749; MUID:99453293; PMID:10521656
A;Accession: T44327
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-346 <AM>A;Residues: 1-346 <AM>A;Residues: 1-346 <AM>A;Residues: 1-346 <AM>A;Residues: 1-346 <AM>A;Residues: 1-346 <AMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:O87156; UNIPARC:UPI00000AF5D0; EMBL;AB012957; NID:g4115688;
A;Experimental source: strain O22
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236
                                                                                                                                                                                                                                                                                                                                      241 NSQCYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNRPKSFVNVHDFNNFDEAIDXIKYLHT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 HPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHKFSTSFMWEYDLH 360
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                                                                                  LRMPLYYDRIHHKABSVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLK 176
                                                                                                                                                                                                                                                                                                          NSQGYGYVTEKIIDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHT 296
                                                                                                                                                                                                                                                                                                                                                                                                                      HPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH--NNPFVFYRDLN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #8equence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44327
                                                                                                                                                                                                                             RGFASFVASNANAPWRNAFYDALNSIEPVTGGGSVRNTLGYKVGNKSEFLSQYKFNLCFE
                                                                                                                                                                                              RGPAS FVASINPNA PKRNA FYDALINS I RPVTGGGS VKNTLGYKVGNKNE FLSQYKFNLCFE
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KPLVSIDD------LRVNYDDLRVNYDRLLQNASPLLELSQNTTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPLVSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYDRLLQNRSPLLELSQNTTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein wbfL [imported] - Vibrio cholerae
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VQTVVQ 339
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Best Local S
Matches 47
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116 YQEAKK--YCG-
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A, Gene: CESP: K08F8.3
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A;Status: prelimary; translated from GB/EMBL/DDBJ
A;Ratus: prelimary; translated from GB/EMBL/DDBJ
A;Residues: 1-451 <WIL>
A;Residues: 1-451 <WIL>
A;Residues: 1-451 <WIL>
A;Residues: clone K08F8
A;Experimental source: clone K08F8
G;Genetics:
                                                                                                                                                                                                                                                                                                      C;Accession: A57596
R;Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.; Je
J. Biol. Chem. 270, 25047-25056, 1995
A;Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q11127; UNIPARC:UP1000004039; GB:U33457; NID:g1039426; PIDN
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 LITTPICWGQLPPLPWASPAPQRLVGVLLWW---EPFRGRGGY-------PKSP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 SDLVFGSPIGAARKILSYONTKRVFYAGENEVPNFN-----LFDYAIGFDELDLRDRY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 PDCSLRFNISGCRLL----TDRAAY-GEAQAVLFHHRDLVKELHDWPPPWGARERTDKA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LHHKAESVNDTTAPY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKPD-----SLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPNAPK-RN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | : | | | : | RIDSDVFVPYGFLYSRSDPTEQPSGLGPQLAR-----KRGLVAWVVSNWNEHQARV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AFYDALNSIEPV----TGGGSVKNTLGYKVGNKNEFLSQYKFNLCFENSQGYGYVTEKI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |: : : |: | | | | : | : |: | | | 330 WRNAFIAGAVPUVLG-PDRANYERFVPRGAFIHVDDFPNAASLAAYLLFLDRNVAVY 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypochetical protein KO8F8.3 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                   alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mouse
NiAlternate names: ELAM-1 ligand fucosyltransferase homolog
C.Species: Mus musculus (house mouse)
C.Species: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -IDAYFSHTIPIYWGSPSVA--KDFNPK-SFVNVHDFKNFDBAIDYVRYLHTHPNAY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LDAFIESASIKKMPLSYP-PLK-IAVANWWGGAEBFKKSAMYFILSQRYTITLHQNPNEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.8%; Score 137.5; DB 2; Length 4 Best Local Similarity 22.4%; Pred. No. 0.04; Matches 80; Conservative 48; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A57596; MUID:96027607; PMID:7559635
A;Accession: A57596
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <GER>
                                                                                              133 E-EDLYNYIISVGKDDEKYYKIYNNKIVPALENN 165
                                                                 283 NFDEAIDYV-----RYLHTHPNAYLDMLYEN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rismye, R. submitted to the EMBL Data Library, October 1995
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8Y294; UNIPARC:UPI0000CCDDCA; GB:BA000019; PIDN:BAB72543.1; A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein alr0585 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTHPNAYL---DMLY 306
                                                                                                                                                                                                                                                               113 RDRYLRMPLYYDRLHHKAESVNDTTA--PYKIKPDSLYTLKKPSHHFKEKHPHLCAVVND 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 -SQYKFNLCFENSQGYGYVTEKIIDAYFSHT-IPIYWGSPSVAKDFNPKSFVNVHDFKNF 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 DIDYHFYUTFENSICEDYVTEKIWKSGYQNTIIPLVLKRKLVEPFVPFNSFIAIDDFKSV 364
                                                                                                                                                                                                                                                                                                                                                                                                             171 ESDPLKRGFASFVASNPNAPKRNAFYDALN---SIEPVTGGGSVKNTLGYKVGNKNEFL- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 SIE------PVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN-SQGYGYVTEKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 YONTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYLRMPLYYDRLHHKAESVNDTTAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 KIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPNAPKRNAFYDALN
                                                                                                                                                                                                                                                                                                                                    207 RPDYINMTLGFR------HDTPAGSPYG-----YTVKLGAKSRKTGQVVDANLVNG
A;Map position: 2
A;Introns: 30/2; 53/3; 133/1; 195/3; 242/3; 277/3; 307/2; 342/3; 382/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75;
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                                                                                                            Query Match 5.7%; Score 134.5; DB 2; Length Best Local Similarity 28.0%; Pred. No. 0.069; Matches 60; Conservative 32; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 DEAIDYVRYLHTHPNAYLDML---YENPLNTLDG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | | : | | : | | : | | | KEMGDYIANYIANNKTAYMBYFEWRHDYKVVFLDG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 EARQLILHKINLLNWLSEFVTQFS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-----NPLNTLDGKAYFYQDLS 324
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113 RDRY-LRMPLYYDRLHHKAESVNDTTAPYKIKPDSL----YTLKKPSHHFKEKHPHLCA 166
                                                                                                                                                                                                                                                                                                    167 VVNDESDPLKRGFASF-----VASNPNAPKRNAF----YDALNSIEPVTGGGSVKNTLGY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 ---NDSLFLSDYVF---ISNT-----IEKQIFDINSDLDLVDYLAKPLRVEINYTISPLA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AKDFNPKSF-----AYLDM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 QKAYEIQSFNRFKNSLLSTLDVDSLNLSDANDVIKNQRYKISYNSLRNSNNNINKIFWKI 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 LYENPLNTLD------GKAYFYQDLSFK-----KILDFF--KTILENDTIYHNN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 KVGNKNEFLSQYKFNLCFENSQGYGYVTEKIIDA----YFSHTIPI---YWGSPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YANDNMLIFGKNNOTNNYNKLYDAYYHLNSFTSFLKKESINENIIDQREKFYLFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYNNL--RADYDRILQNRSPLIE--LSQNT-----TFKIYHK-----AYHKSLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 PFVFYRDLNEPLVSIDDLRADYNNLRADYNNL-----
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Best Local Similarity 19.6*
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 LRAIRRWVK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587 IKSİHPSLK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387
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A;Gene: PFB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: Embryonal carcinoma F9 cells
C, Superfamily: galactoside 3 (4)-L-fucosyltransferase
C, Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F;1-3 Domain: intracellular #status predicted <INT>
F;24-49/Domain: transmembrane #status predicted <IRM>
F;84,185/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
Cispecies: Mycoplasma pulmonis
Cispecies: Mycoplasma pulmonis
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
CiAccession: 690587
Richambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Ree. 29, 145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                 C;Accession: JC4591
V; Muramatsu, T.
J. Biochem. 119, 302-308, 1996
A;Title: Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene
A;Reference number: JC4591; MUID:97037075; PMID:8882722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LHHKAESVNDTTAPY 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 KIKPD-----SLYTLKKPSHHFKEKHPHLCAVVNDESDFLKRGFASFVASNPNAPKRNA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
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                                                       C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | : : | : | : | : | : | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 | 3.2 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.4%; Score 128.5; DB 2; Length 400; Best Local Similarity 21.8%; Pred. No. 0.15; Matches 78; Conservative 49; Mismatches 131; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-400 <OZA>
A;Cross-references: UNIPARC:UP1000016CBA5; DDBJ:D63379
            alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse
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A,Status: preliminary
A,Molecule type: DNA
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A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                    A; Accession: JC4591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
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Rigardher, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Frertea, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Reference number: a71602
A;Reference number: are acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA |
A,Residues: 1-3973 <GAR>
A,Cross-references: UNIPROT:096204; UNIPARC:UP10000179222; GB:AE001402; GB:AE001362; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2016 PDIIMCILEQYIAHYNYYIXKGKAMDVFFNKLKILMLSLHFVNSIYFNIFCDDINABIKR 2075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 ITLHONPNEPSDLVFGSPIGAARKILSYQNTK------RVFYAGENEVPNFNLFDYAIG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPNAPKRN-----A 194
hypothetical protein PFB0555c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: B71612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 FD-ELDLRDRYLRMPLYY-----DRLHHKAESVN--------DTTAPYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%; Score 126.5; DB 2; Length 3973;
19.6%; Pred. No. 4.9;
ative 68; Mismatches 160; Indels 153;
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A;Gene: PFB0555c
C;Superfamily: Plasmodium falciparum hypothetical protein PFB0555c
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58 QNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNL----FDYAIGFDEL-DL 112

151; Indels 149;

DB 2; Length 789;

5.4%; Score 127.5; DB 20.9%; Pred. No. 0.45; Live 87; Mismatches 1

Conservative

Local Similarity ses 102; Conserv

Best Loca

Query Match

G90587

OY   23 PPLKIAVANWM	Db 215GDPPSGL Qy 211 VKNTLGYKVGNKN Db 269 PVPBIGLL Qy 268 KDFWF-SFVNVH	RESULT 15 H96742 H96742 C;Species: Arabidopsis C;Date: 02-Mar-2001 #se C;Date: 02-Mar-2001 #se C;Date: 02-Mar-2001 #se C;Date: 02-Mar-2001 #se C;Date: 03-Mar-2001 #se C;Date: 04-Mar-2001 #se C;Date: 04-Mar-2001 #se Nature 408, 816-820, 20 A;Authors: Hunter, J.L. C;A.; Li, J.H.; Li, Y.; Rizzo, M.; Rooney, T. Rizzo, M.; Wu, D.; Yu, Rizzo, M.; Wu, D.; Yu, Rizzo, M.; Wu, D.; Yu, A;Attle: Sequence and G A;Reference number: A86 A;Reference	A; Molecule type: DNA A; Residues: 1-393 <sto> A; Cross-references: UNIPROT C; Genetics: F17M19.14 A; Map position: 1 Query Match Best Local Similarity 3 Matches 29; Conservati</sto>	Oy   226 ISOYKFNLCFENS 	
Qy         195 FYDALMSIEPVTGGGSVKNTIG-YKVGNKNEFLSQYKFNL 233               :   :	2297 LINDEYNNFLDNHKCKRKRKFINT 387 DYNN		A; Reference number: A40976; MUD: 91373370; PMID: 1716630 A; Recension: A40976 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-86, P', 88-405 < LOW> A; Cross-references: UNIPARC: UPI0000012ADA6; GB: M65030; NID: G182791; PIDN: AAA92977.1; P A; Cross-references: UNIPARC: UPI000012ADA6; GB: M65030; NID: G182791; PIDN: AAA92977.1; P A; Cross-references: Muller, W.A.; Stanley, P. J. Biol. Chem. 266, 21777-21783, 1991 A; Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but A; Reference number: A41202; MUID: 92042084; PMID: 1718983	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-240, 'D',242-400 <kum> A;Residues: 1-240, 'D',242-400 <kum> A;Cross-references: UNIPARC:UPI000016B3BD; GB:S65161; NID:g239005; PIDN:AAB20349.1; P C;Genetics: C;Genetics: A;Gene: GDB:FUT4; CD15; FCT3A; FUC-TIV A;Cross-references: GDB:131563; OMIM:104230 A;Map position: 11q21-11q21 C;Superfamily: galactoside 3(4)-L-fucosyltransferase C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase F;1-48)Domain: signal sequence #status predicted <nat> F;91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted F;91,190/Binding site: carbohydrate (Asn) (covalent)</nat></kum></kum>	Query Match 5.3%; Score 124.5; DB 2; Length 405; Best Local Similarity 22.7%; Pred. No. 0.3; Matches 76; Conservative 43; Mismatches 123; Indels 93; Gaps 18;

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Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; A.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, wley, D.; Sakano, H. Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I raser, C.M.; Venter, J.C.; Davis, R.W. lysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DT:Q9C8W3; UNIPARC:UPI000004845A; GB:AE005173; NID:g6978923; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
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                                                                                                                                                                                                                                                                    AAR----KILSYQNTKRVFYAGENEVP-----NFNLFDYAI 105
                                                                                                               RMPLYYDRIHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLC 165
    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.14 [imported] - Arabidopsis thaliana
11iana (mouse-ear cress)
ence_revision 02-Mar-2001 #text_change 09-Jul-2004
--GGAEEPKK----SAMYFILSQRYTITLHQNPNEPS-----DLVF
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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면다		MAY-1999, FEB-2006,	sequent entry	ce ver	Bic Dia	n 1.			
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888		Bacteria; Proteob Helicobacteraceae NCBI TaxID-85963:	teobaci ceae; I	teria; Helico	Bac	silonproteol ter.	oacteria; Campy	lobacterales;	
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RA		Gibson R., Merberg D., Trust T.J.;	rberg	D., Mi	118	S.D., Jian	g Q., Taylor D.	., Vovis	
RT		"Genomic sequ gastric patho	sequence co	comparison [elicobacte	son	c sequence comparison of two unrelated pathogen Helicobacter pylori.";	slated isolates	of the human	
를 당		ure 397:17	6-180(:	1999).	i				
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S K D S	A PAN COM	erPro; IPR THER; PTHR plete prot UENCE 43	001503, 111929; eome; ( 6 AA;	Glyc Glyco Glycos Glycos 50699	폴片다	rans 10. ; ans 10; 1. ransferase; ; 1DB2066AI	InterPro; IPR001503; GLyco trans 10.; PANTHER, PTHR11929; GLyco_trans_10; 1. Complete proteome; Glycosyltransferase; Transferase. SEQUENCE 436 AA; 50699 MW; IDB2066AE98FA61E CRC64;		
	Query Match Best Local Matches 38	Match Local Simil Les 384; C	86.3%; Similarity 86.5%; 4; Conservative 2	86.3 86.5 ttive	ر. مو مو	Score 2039; Pred. No. 3.3 25; Mismatches	; DB 2; Length 3.3e-130; nes 23; Indels	436; s 12; Gaps	ω,
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0006486; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

Complete proteome; Glycosylationsferase; Transferase.

SEQUENCE 476 AA; 55927 MW; 32BFFDBBD36E1F74 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
Smith H.O., Fraser C.M., Venter J.C.;
               180 RGFASFVASNBNAPIRNAFYDALNSIEPVTGGSVKNTLGYNVKNKSEFLSQYKFNLCFE
                                                                       300 HPNAYLDMLYENPLATILDGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIFYRDLNEP
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                                                        NSQGYGYVTEKIIDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHT
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                           476 AA.
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Best Local Sim: Matches 374;

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GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0016797; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:0016797; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:0016797; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:0016797; F:transferase activity, transferring glycosyl. . .; IEA.

Glycosyltransferase; Transferase.

Glycosyltransferase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NCTC 11639; MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357; Ge Z., Chan N.W.C., Palcic M.M., Taylor D.E.; "Cloning and heterologous expression of an alphal,3-fucosyltransferase gene from the gaetric pathogen Helicobacter pylori."; J. Biol. Chem. 272:21357-21363(1997).
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1 MFQPLLDAPIESASIEKMVSKSPPPPLKIAVANWWGDEBIKEFKKSVLYFILSQRYAITL
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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78.5%; Pred. No. 8.3e-126;
iive 32; Mismatches 33;
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Distributed under the Creative Commons Attribution-NoDerivs License
                        1 MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKNSVLYFILSQRYTITLH
                                                                                                                           GFASFVASNPNAPKRNAFYDALNSIBPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN
                                                                                                                                                  GPAS FVASNPNAPIRNAFYDALNS I EPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCFEN
                                                                                                                                                                            SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH
                                                                          RMPLYYDR1HHKAESVNDTTAPYKI KPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WICLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Ulia-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA (1,3)-FUCOSYLTRANSFERASE.
Name-fuct; ORFNames-jhp_0596 (Campylobacter pylori J99).
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                               ------RLLQNRSPLLELSQNTTFKIYHKAYHKSLPLLRAIRRWVKKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            two unrelated isolates of the human
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GO; GO:0016020; C:membrane; IRA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

GO; GO:001686; P:protein amino acid glycosylation; IEA.

InterPro; IPR001503; Glyco trans 10.

PANTHER; PTHR11929; Glyco-trans 10.

COMPLETE Proteome; Glycosyltransferase; Transferase.

SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;
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                                                                                                                                                                                                                                                                              VSIDDLRADYNNLRADYNNLRADYNNLRADYNNLRADYD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.0%;
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Best Local Similarity
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                                                                                       1 MFQPLLDAYTDSTRLDETDYK-PPLNIALANWWPLDKRESKGFRRFILYFILSQRYTITL
                                                                                                                                                                                             60 HQNPNEPSDLVFGSPIGSARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFRDRY
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                                                     MFQPLLDAFIESASIKKMPLSYPPLKIAVANWW----GGAEEFKKSAMYFILSQRYTITL
  Gaps
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"Molecular Cloning and Functional Expression of a Novel Helicobacter
pylori (alpha-1, 4 Fucosyltransferase.";
Glycobiology 15:1076-1083(2005).
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
19;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:001686; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
FANTHER; PTHR11929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;
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PubMed=16000696; DOI=10.1093/glycob/cwj004;
  Mismatches
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  34;
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Q6ST35;
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GO:0006486; P:protein amino acid glycosylation; IEA
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                                                                                                                          LYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFA 180
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GO:0008417; F:fucosyltransferase activity; IEA.
GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
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                              1 MFQPLLDAYIDSTRLDETDYK-PPLKIAVANWWGGVEEFKKSTLYFILSQRYTITLHRNP
                                                                                   120 LYYAHIHYEAELVNDTTSPYXIKDNSLYALKKPSHHPKENHPNLCAVVNNESDPLKRGFA
                                                                                                                                                                                              SFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTIGYNVKNKNEFLSQYKFNLCFENSQG
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|SIDD-----LRINYDDLRINYDDLRINYERLLQNASPLLELSQNTSFKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlawage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,

Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,

Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,

Dougherty B.A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,

Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,

Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,

Rathey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D.,

Smith H.O., Fraser C.M., Venter J.C.;

The complete genome sequence of the gastric pathogen Helicobacter
              MPQPLLDAFIESASIKKMPLSYPPLKIAVANWWGGAEEFKKSAMYFILSQRYTITLHQNP
                                                                                                                                                                                SFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFENSQG
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998, integrated into UniProtKB/TrEMBL 01-JAN-1998, sequence version 1. 07-FEB-2006, entry version 24. Fucosyltransferase.
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025142;
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Distributed under the Creative Commons Attribution-NoDerivs License
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"Cloning and characterization of the alpha(1,3/4) fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
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MEDLINE=20138242; PubMed=10671538; DOI=10,1074/jbc.275.7.4988;
                                                                                                                             2; Length 425;
                                                                                                                                                                            Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10; Transferase.
Complete Protecome; Glycosyltransferase; Transferase.
SEQUENCE 425 AA; 49329 MW; 1182AP180D124A34 CRC64;
                                                                                                                        Query Match 79.6%; Score 1879.5; DB 2; Best Local Similarity 80.9%; Pred. No. 2.2e-119; Matches 361; Conservative 24; Mismatches 34;
                                                                                                                                                                                                                              1 MFQPLLDAFIESASIKKMPLSY -- PPLKIAVANWWGGAE
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Biol. Chem. 275:4988-4994 (2000)
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Name=fucTa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9L8S4_HELPY PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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Bacteroidaceae; Bacteroides.
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QSL9S6;
                                                                                                                                                        Matches 280; Conservative
                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                1 MFQPLLDAFIDSTHLDE-TTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIIL
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
MATLIN S.L., Edbrooke M.R., Hodgman T.C., van den Bijnden D.H.,
Bird M.I.;
"Lewis X biosynthesis in Helicobacter pylori. Molecular cloning
EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008641; F:fucomyltransferame activity; IEA.
GO; GO:0016757; F:tannsferame activity, transferring glycosyl.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco, trans 10.
PANTHER; PTHA11929; Glyco_trans 10.
Glycosyltransferame; Transferame.
Glycosyltransferame; Transferame.
SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;
                                                                                                                                                       31;
                                                                                                                               DB 2; Length 462;
                                                                                                                            74.9%; Score 1769.5; DB 2; Length
72.3%; Pred. No. 7.4e-112;
ive 43; Mismatches 55; Indels
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J. Biol. Chem. 272:21349-21356(1997).
                                                                                                                              Query Match 72.3
Best Local Similarity 72.3
Matches 336; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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PubMed=15746427; DOI=10.1126/science.1107008;
Cerdeno-Tarraga A.-M., Partick S., Crossman L.C., Blakely G.,
Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
Line A., Lord A., Norbertczak H., Ormond D., Price C.,
Rabbinowitsch B., Norbertcak J., Barrell B.G., Parkhill J.;
"Extensive DNA inversions in the B. fragilis genome control variable
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
EMBL, AF006039, AAB93985.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:tucosyltransferase activity; IEA.
GO; GO:001677; F:transferase activity, transferring glycosyl.
GO; GO:0016486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
FANTHER; PTHR1929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 333 AA; 39154 MW; CFFCBIAC12TE0A8C CRC64;
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Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                      Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                           16; Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:000686; P:protein amino acid glycosylation; IEA.
InterPro; IPR002105; Dockerin_1.
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21-JUN-2005, sequence version 1.
07-FEB-2006, entry version 6.
Putative LPS biosynthesis related glycosyltransferase.
OrderedLocusNames=BP9460;
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                                                                                                                                                                                                                                                                                                                                      Score 1509; DB 2;
Pred. No. 2.5e-94;
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94.1%; Pred. No. 4...
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-EKLENFLLH----IF----NOPL 290
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OZIE19;
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BioCyc; HHEP235279; HH1776-MONOMER; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016727; F:tucnsferase activity; IEA.
GO; GO:0016777; F:tucnsferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016787; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016787; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016787; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016787; F:transferase activity, transferase.
GO; GO:0016787; F:transferase; Transferase.
SEQUENCE 359 AA; 42275 MW; B01B3FBBBC82D463 CRC64;
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                                                                                                                                                                                     13 MKKIYLKF-----VDFWDGFDTISN----FIVDALSIQYEVVL---SNEP-DYLFYSC
                                                                                                                                                                                                                                                                                             127 HHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASN
                                                                                                                                                                                                                                                                                                                                                            187 PN--APKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFENSQGYGYV
                                                                                                                                                                 15 IKKMPLSYPPLKIAVANWWGGAEEFKKSAMYFI---LSQRYTITLHQNPNEPSDLVFGSP
                                                                                                                                                                                                                                                                                                                                                                                                                          245 TEKIIDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTHPNAYLDM
                                                                                                                                  Gaps
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MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
Suerbaum S., Josenhard C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Weber J., Prosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
Helicobacter hepaticus.",
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                  74;
                                                                                                 Query Match 18.8%; Score 445; DB 2; Length 331; Best Local Similarity 35.4%; Pred. No. 5.2e-22; Matches 118; Conservative 46; Mismatches 95; Indels
                                                                   331 AA; 39181 MW; 679FA409DF8CB864 CRC64;
InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10; 1.
PROSITE; PS00448; CLOS_CELIULOSOME_RPT; UNKNOWN_1.
Complete proteome; Transferase.
SEQUENCE 331 AA; 39181 MW; 679FA409DF8CB864 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 LYENPLNTLDGKAYFYQDLSFKK-ILDFFKTIL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 L-EKP--WLLDKTY----LDWKQLLLNFINNIM 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003, integrated into UniProtKB/TrEMBL
01-0CT-2003, sequence version 1.
07-FEB-2006, entry version 12.
Alpha-1,3-fucosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter hepaticus.
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Q7VFA1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272
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                                                                                                                                                                                                                                                                                                                                                                                 KSFVNVHDFKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFF 332
                                                                                                            41 KSAMYFILSQRYTITLHQNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNL 100
                                                                                                                                                                                                                                                                                       111
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                                                                                                                                                                                                                              101 FDYAIGFDELDLRDRYLRMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PVRLDFVDFWPGFDR-RNNVLLDVLRTRFAVEVVDDP----DFVFFANFG--WRHWRYRC
                                                                                                                                                                                                                                                                  24 PLKIAVANWWGGAEEFKKSAMYFILSQRYTITLHQNPNEPSDLVFGSPIGAARKILSYQN
                                                                                                                                                23 KGKIVALLEQHYELIL---TNKDPDYIFYSCMGFEH--LNY-NKVRIPATGENLRADFNF
                                                                                                                                                                                                                                                                                                                                                161 HPHLCAVVNDESDPLKRGFASFVASNPNAPK-RNAFYDALNSIEPVTGGGSVKNTLGYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNKNEFLSQYKFNLCFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVA-----KDFNP
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US DOE Joint Genome Institute;
US DOE Joint Genome Institute;
Copeland A., Lucas B., Lapidus A., Barry K., Detter J.C., Glavina T Copeland M., Israni S., Pitluck S., Brettin T., Bruce D., Han C., Tapia R., Gilna P., Kiss H., Schmutz J., Larimer F., Land M., Kyrpides N., Anderson I., Sanford R.A., Ritalahti K.M., Thomas H.S. Rirby J.R., Zhulin I.B., Loeffler F.E., Richardson P.;
"Complete sequence of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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                                                            65;
   Length 359;
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Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Myxococcaceae, Anaeromyxobacter.
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07-MAR-2006, entry version 1.
Putative LPS biosynthesis related glycosyltransferase
ORFNames-Adel 3056,
                                                            96;
18.3%; Score 431.5; DB 2; 34.8%; Pred. No. 4.8e-21;
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                           Best Local Similarity 34:8%; Fred. No. 4.8e-
Matches 113; Conservative 51; Mismatches
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Coper J., Hardran, Song J., Olsen R., Rajandream M.A.,
Sichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
Sucyang R., Berthann M., Song J., Olsen R., Szaffenski K., Xu Q.,
Sucyang B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey F.,
Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey F.,
Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey F.,
Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey F.,
Bankier A.T., Lehmann R., Hall N., Anjard C., Hemphill L., Bason N.,
Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Farbrother P., Desany B., Just B., Morio T., Rost R., Churcher C.M.,
Coper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,
Anjut R.A., Loulseged H., Hurnandez J., Rabbinowitsch E., Steffen D.,
Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
Tivey A., Suyano S., White B., Walker D., Woodward J.R., Winckler T.,
Tanka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
Kaya R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
                      263
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144 PDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPNAPKRNAFYDALNSIE 203
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                                                                                                    264 PSVAKDFNPKSFVNVHDFKNPDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQDL
                                                                                                                                                                           PVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFENSQGYGYVTEKI IDAYFSHTIPIYWGS
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PANTHER; PTHR11929, Glyco trans 10; 1.
Glycosyltransferase; Golgī stack; Hypothetical protein; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 435:43-57(2005).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome of the social amoeba Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0016020; C:membrane; IEA.
GO:0008417; F:fucosyltransferase activity; IEA.
GO:0006486; P:protein amino acid glycosylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 AA; 54815 MW; 444843FFBAEF6D77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                             462 AA.
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2005, sequence version 1.
07-MAR-2006, entry version 5.
Hypothetical protein.
ORFNames=DDB0186041,
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                    324 SPKKILDPPKTI 335
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Q54PJ9;
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Length 462;

Score 210; DB 2;

8.98;

Query Match

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Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
A bankier A.T., Lehmann R., Hamilan N., Davies R., Gaudet P., Fey P.,
Bilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Rerhornou A., Nie S., Van Driessche N., Cronin A., Goodhead I.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindaay R.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindaay R.,
Hauser H., Vames K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Sugano S., Mite B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schleicher M., Walnstock G., Rosenthal A., Cox E.C.,
Milians J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
"The genome of the social amoeba Dictyostelium discoideum.";
Nature O:O.0(2005).
                                                                                                                                                               184 BFDKDCFEFFNFKVSFBSQSDIRMGFDTPSSSAYKLYNKLTIDBIAKIQTQFKLE---Y 239
                                                                                    98 -----FNLFDYAIGFD-ELDLRDRYLRMPLYYDRLHHK--AESVNDTTAPYKIKPDSLY 148
                                                                                                                                                                                                                        149 TLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPNAPKRNAFYDALNSIEPVTGG 208
                                                                                                                                                                                                                                                                                                       GS-----VKNTLGYKVGN----KNEFLSQYKFNLCFENSQGYGYVTEKIIDAYFSHTIP 258
                                                                                                                                                                                                                                                                                                                              288 GKCLKNMPTSNFLSRGSGDPFERKRLPITRYKFTIVFENSICKDYVSEKVLDALIAGSVP 347
                                                                                                                                                                                                                                                                                                                                                                                   259 IYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAY 318
                                                                                                                                                                                                                                             240 QVMK---HNNTLQPH-----QKSIPLANWPCTNCNSHSN---RNEYVQELMKFIVVDSF 287
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                                                           45 YFILSQRYTITLHQNPNEPSDLVFGS----PIGAARKILSYQNTKRVFYAGENEVPN---
                      Gaps
                      68;
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  ; Pred. No. 7.6e-06;
64; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 PYQDLSFKKILDPFKTILENDTIYHNNPFVFYRDLNEPLV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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GO:0008417; F:fucosyltransferase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 AA.
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23.8%;
                      81; Conservative
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    Best Local Similarity
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                      Matches
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Best Local Similarity 37.39
Matches 47; Conservative
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087156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDBAIDYVRYLHTHPNAYLDMLY 306
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                                                                                                                                                                                                                                                                                                                                                                                                  215 -----LGYKVGNKNEF-------LSQYKFNLCFENSQGYGYVTE 246
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Rosembl; ENSCINGO000006882; Ciona intestinalis.

GO; GO:0005795; C:Golgi stack: IEA.

GO; GO:0016020; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl...;

GO; GO:0016757; F:transferase activity, transferring glycosyl...;

GO; GO:0016757; F:transferase activity, transferring glycosyl...;

GO; GO:0016757; F:transferase activity, transferring glycosyl...;

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

R InterPro; IPR001005; Myb_DNA.bd.

R PANTHER; PTHX11929; Glyco_trans_10; 1.

R PROSITE; PS00037; MYB_1; UNKNOWN_1.

R PROSITE; PS00037; MYB_1; UNKNOWN_1.

R Glycosyltransferase; Golgi stack; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
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8.2%; Score 193.5; DB 2; Length 417;
Best Local Similarity 24.8%; Pred. No. 8.8e-05;
Matches 82; Conservative 49; Mismatches 89; Indels 111;
                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                              167 VVNDESDPL----KRGFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candelier J.J., Martinez-Duncker I., Oriol R., Mollicone R., Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   Query Match 8.3%; Score 195; DB 2; Length 665; Best Local Similarity 25.5%; Pred. No. 0.00013; Matches 68; Conservative 31; Mismatches 82; Indels
GO; GO:0006486; P:protein amino acid glycosylation; IEA. InterPro; IPR013320; Cona_like_subgrp. InterPro; IPR001503; Glyco_trans_10. PANTHER; PTHR1929; Glyco_trans_10; 1.
                                                                                                    Hypothetical protein.
SEQUENCE 665 AA; 76223 MW; D42588B008EBDB46 CRC64;
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07-FEB-2006, entry version 14.
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QBGNA8;
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                                                                                                                                                                                                                                      209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 -SVAKDENPKSFVNVHDFKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQDL 323
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                                                         126 LINGGPDPKSKK----RNOKYVYFDLE---PTWALQGMNYSIGENGFFNWTMSYKRTSSI
                                                                                                                   ------FDELDLR----DRYLRMPLYYORLHHKAESVNDTTAPYKIKPDSLY---T
                                                                                                                                                    150 LKKPSHHPKEKHPHLCAVVNDESDPLKRGFASFVASNPNAPKRNAFYDALNSIEPVTGGG
                                                                                                                                                                                                                                                                        210 SVKNTLGYKVGNKNEFLSQYKFNLCFENSQGY---GYVTEKI-IDAYFSHTIPIYWGSP-
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Vibrionaceae; Vibrio.
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66 LVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNL--FDYAIG-----
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

InterPro; IPR001503; Glyco_trans 10.

PANTHER; PHR11929; Glyco_trans 10, 1.

SEQUENCE 346 AA; 40359 MW; 28690BC3FEFFDA7F CRC64;
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1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

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US-09-092-315-2
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Maximum Match 100%
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Sequence 6, Appli Sequence 13, Appl Sequence 13, Appl Sequence 16, Appl Sequence 2, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 9, Appli Sequence 9, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 14, Appli		Length 440; Indels 0; Gaps 0; SAMYPILSORYTITLHONP 60	YAIGFDELDLRDRYLRMP 120 YAIGFDELDLRDRYLRMP 120 YHLCAVVNDESDPLKRGFA 180 HHCAVVNDESDPLKRGFA 180	CMEFLSQYKFNLCFENSQG 240
US-10-189-977A-6 US-10-392-098A-6 US-09-092-315-13 US-10-080-960-18 US-10-080-960-2 US-09-092-315-11 US-09-733-524A-11 US-10-189-977A-11 US-09-733-524A-11 US-09-733-246-8 US-09-533-246-8 US-08-555-058A-8 US-08-555-058A-8 US-08-696-731-8 US-09-042-531-8	ALIGNMENTS 092315 3-FUCOSYLTRANFERASE US/09/092,315 -05 18 Version 3.0	Score 2362; DB 2; Pred. No. 7.9e-224; 0; Mismatches 0; PLSYPPLKIAVANWWGGAEEFKK	NEPSDLVFGSPIGAARKILSYQNTXRVFYAGENEVPRFNLFDYAIGFDELDLRDRYLRWP	FVASNPKA PKRNA FYDALNSI EBVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFENSOG 
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                                                                                                                                                              Sequence 3, Application US/09733524A

Fatent No. 65429B

GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: WURBER: US/09/733,524A

CURRENT APPLICATION NUMBER: US 09/092,315
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 27

SOOFWARE: FastSEQ for Windows Version 4.0
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                                                                  ORGANISM: Helicobacter pylori
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RESULT 3 US-10-189-977A-3

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APPLICANT: TAYLOR Diane E.

APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCCSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPERSING THEM (amended)
TITLE OF INVENTION: EXPERSING THEM (amended)
TITLE OF INVENTION: EXPERSING THEM (amended)
TITLE OF INVENTION: WHERE: US/0.02
CURRENT APPLICATION NUMBER: US/0.9/73,524
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 2000-12-0.07
PRIOR FILING DATE: 1998-06-05
PRIOR PRILING DATE: 1998-06-05
PRIOR PILING DATE: 1997-06-06
NUMBER: OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 7029891
GENERAL INFORMATION
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/392,098A
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TYPE: PRT
ORGANISM: Helicobacter pylori
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US-09-092-315-8
LENGTH: 454
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                                                                                                                                                                                                                                                                                                                                                   Length 440;
                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: H. pylori strain UA802
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpPucT)
US-10-392-098A-3
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Sequence 8, Application US/09092315

Fatent No. 639937

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Ge. Zhongming

TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE

FILE REFERENCE: 07254/049001

CURRENT APPLICATION NUMBER: US/09/092,315

CURRENT PILING DATE: 1998-06-05

BERLIER APPLICATION NUMBER: US 60/048,857

BARLIER FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2362; DB 3;
100.0%; Pred. No. 7.9e-224;
tive 0; Mismatches 0;
          PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-06-05
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.1
LENGTH: 440
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2003-03-17
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                  Matches 440; Conservative
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Best Local Similarity
CURRENT FILING DATE:
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GENERAL INFORMATION:
APPLICANT: Taylor, Diane B.
APPLICANT: G., Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/733,524A
CURRENT FILING DATE: 2000-12-07
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                                                           Gaps
                                                     17;
Length 454;
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  ;; Score 2015.5; DB 2
;; Pred. No. 1.1e-189;
34; Mismatches 26;
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09733524A Patent No. 6534298
  Query Match
Best Local Similarity 83.0%;
Matches 377; Conservative 3.
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178 GFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYKVGNKNEFLSQYKFNLCFEN
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398 -000420US
CURRENT APPLICATION NUMBER: US/10/392,098A
CURRENT APPLICATION NUMBER: US/10/319
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1090-06-05
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ORGANISM: Helicobacter pylori
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Sequence 8, Application US/10189977A

Patent No. 6962806

GENERAL INFORMATION:
PAPPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: FUCOSYLFRANSFERASE AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US/09/733,524

PRIOR APPLICATION NUMBER: US 60/048,857

PRIOR APPLICATION NUMBER: US 60/048,857

PRIOR PILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARRE: FastESEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 454
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                                                   QNPNEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYL 117
                                                                             RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR 177
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MFQPLLDAFIESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSTLYFILSQHYTITLH 60
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85.3%; Score 2015.5; DB 2
Best Local Similarity 83.0%; Pred. No. 1.1e-189;
Matches 377; Conservative 34; Mismatches 26;
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ORGANISM: Helicobacter pylori
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241 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKOFNPKSFVNVHDFNNFDEAIDYVRYLHTH
                                                                                                                                 PNAYLOMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNEPL
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                                                       SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH
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Best Local Similarity 83.0%; Pred. No. 1.1e-189;
Matches 377; Conservative 34; Mismatches 26; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: H. pylori strain NCTC11637; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT) US-10-392-098A-8
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Indels
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84.6%; Score 1999; DB 2;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28;
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US-09-733-524A-2
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                                                                                                                                                                                                                                                                                                         GENERAL INTORNATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
ITILE OF INVERTION: ALPHA-1, 3-FUCOSYLTRANFERASE;
FILE REFERENCE: 07254/04901
CURRENT PILING DATE: 1990-06-05
CURRENT PILING DATE: 1990-06-05
FARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTESQ for Windows Version 3.0
SSEQ ID NO 2
LENGTH: 486
                                                                                                                  VSI DDLRADYNNLRADYNNLRADYNNLRADYD-
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; Sequence 2, Application US/09092315
; Patent No. 6399337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Helicobacter pylori
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Matches 377; Conservative
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Sequence 2, Application US/09733524A

Patent No. 6534298

GENERAL INPORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongwing
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: 000-12-07
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 0724-049002
FILE REPRENCE: 0724-049002
FILE REPRENCE: 0799-06-05
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR PRICE FABSEQ for Windows Version 4.0
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                       GENERAL INCORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/189,977A
FILE REFERENCE: 07254-049002
CURRENT FILING DATE: 2002-03-07
FRIOR APPLICATION NUMBER: US/09/733,524
FRIOR PLILING DATE: 2000-12-07
FRIOR PLILING DATE: 1998-06-05
FRIOR FILING DATE: 1998-06-05
FRIOR FILING DATE: 1998-06-06
FRIOR FILING DATE: 1997-06-06
FRIOR FILING DATE: 1997-06-06
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 486
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 486;
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84.6%; Score 1999; DB 2;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28;
Sequence 2, Application US/10189977A
Patent No. 6962806

    TYPE: PRT
    ORGANISM: Helicobacter pylori
US-10-189-977A-2

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58 ONPNEPSDLVFGSPIGAARKILSYONTKRVFYAGENBVPNFNLFDYAIGFDELDLRDRYL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
. OTHER INFORMATION: H. pylori strain UA1182
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-0988-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 486;
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APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REPERENCE: 017399-0042005
CURRENT APPLICATION NUMBER: US/10/392,098A
CURRENT FILING DATE: 2003-03-17
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALENT IN VET: 2.1
SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

84.6%; Score 1999; DB 3;
Best Local Similarity 77.6%; Pred. No. 5.2e-188;
Matches 377; Conservative 35; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Taylor, Diane
APPLICANT: Ge, Zhongming
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Sequence 2, Application US/10392098A
Patent No. 7025891
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.

US-10-392-098A-2

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Sequence 1, Application US/10189977A Patent No. 6962806
ORGANISM: Helicobacter pylori
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US-10-189-977A-1
                                                                                                             Query Match
Best Local Similarity 80.8%
Matches 375; Conservative
                   ; OKGANISM: HE.
US-09-733-524A-1
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Sequence 1, Application US/09733524A

Patent No. 6534298

GENERAL INPORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/09/733,524A

CURRENT FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ONPNEPSDLVFGSPIGAARKILSYONTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYL 117
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80.8%; Pred. No. 1.8e-186;
iive 32; Mismatches 33;
   TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
                                   FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
FEARLIER APPLICATION NUMBER: US 60/048,857
EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.84
Matches 375; Conservative
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LENGTH: 464
TYPE: PRT
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PATCHEAL NO. 932800

PATCHICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE GP. INVENTION: WUCLERC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: BEAPERSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: 10724-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT PILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-07

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FABLSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 464
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                                          Gaps
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  Length 464;
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                                          Indels
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                                          33;
84.0%; Score 1983; DB 2;
80.8%; Pred. No. 1.8e-186;
tive 32; Mismatches 33;
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Best Local Similarity 80.8%; Pred. No. 1.8e-186;
Matches 375; Conservative 32; Mismatches 33;
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RMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKR 177
1 MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKNSVLYFILSQRYTITLH 60
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Search completed: August 11, 2006, 19:47:32 Job time : 32.1639 secs

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US-10-120-319-3
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1960.5
1924.5
1879.5
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1961
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1742.5
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                                                            August 11, 2006, 19:46:14; Search time 107.213 Seconds (without alignments) 1901.022 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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1 MFQPLLDAFIESASIKKMPL.....YHKSLPLLRAIRRWVKKLGL
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GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-189-977-3
US-10-392-997-3
US-10-1392-997-3
US-10-120-319-8
US-10-189-977-8
US-10-189-977-2
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US-10-392-098-2
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US-10-189-977-1
US-10-189-977-5
US-10-189-977-5
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1982.5
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6, Appli
12, Appli
16, Appl
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US-09-733-524-17
US-10-1335-977-8558
US-10-133-977-6
US-10-189-877-6
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Sequence 3, Application US/10120319;
Publication No. US20020164749A1
GENERAL INPORMATION:
APPLICANT: TAYLOr, Diane E.
APPLICANT: TAYLOr, Diane E.
FILE REFERENCE: 07254/049001;
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR PLILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FARLSER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FARLSER FILING DATE: 1997-06-06
SOFTWARE: FARLSER FILING DATE: 10 NO 3
                                                                                                                                                                                                                                                                                                                                                                                                          US 60/048,857
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1 MFQPLLDAPIESASIKKMPLSYPPLKIAVANWWGGAEEFKKSAMYFILSQRYTITLHONP ö Length 440; Indels 100.0%; Score 2362; DB 4; 100.0%; Pred. No. 4.1e-192; ative 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 440; Conservative

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61 NEPSDLVPGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLADRYLRMP 120 180 240 9 1 MPOPLEDAFIESASIKGOMPLSYPPLKIAVANWWGGAEEFKKSAMYPILSQRYTITLHONP NEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYLRMP SFVASNPNA PKRNA FYDALINS I BPVTGGGS VKNTLGYKVGNKNE FLSQYKFNLCFENSQG YGYVTEKI IDAYFSHTI PIYMGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTHPNA 241 YGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTHPNA LYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFKBKHPHLCAVVNDESDPLKRGFA

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Best Local Similarity 100.0%; Pred. No. 4.
Matches 440; Conservative 0; Mismarchoo
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                             440
                                       TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                  LENGTH: 440
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Sequence 3, Application US/10392098

RESULT 3 US-10-392-098-3

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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REPRESSING THEM (amended)
FILE REPRESSING THEM (amended)
CURRENT APPLICATION NUMBER: US/10/392,098
CURRENT PILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/99/733,524A
PRIOR PILING DATE: 1998-66-05
PRIOR PILING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NO 3
LENGTH: 440
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; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Hezila, Daniel James
; APPLICANT: Bezila, Daniel James
; APPLICANT: Governors of the University of Alberta
; APPLICANT: House Technologies, Inc.
; APPLICANT: House Technologies
; APPLICANT: House Technologies
; TITLE OF INVENTION: H. Pylori Fucosyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 2362; DB 4; Best Local Similarity 100.0%; Pred. No. 4.1e-192; Matches 440; Conservative 0; Mismatches 0;
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Publication No. US20030166212A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
US-10-392-098-3
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ORGANISM: Helicobacter Pylori fucosyltransferase
                                  NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: Strain 802 from UA802
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Publication No. US20020164749A1
GENERAL INFORMATION:
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Matches 438, Conservative
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Matches 377; Conservative
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US-09-733-524-3
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is Sequence 3, Application US/09733524

j Sequence 3, Application US/09733524

j Sequence 3, Application US/09733524

j Patent No. US20020068347A1

j Patent No. US20020068347A1

j APPLICANT: The Governers of the University of Alberta, a Canada Corporation

j APPLICANT: The Governers of the University of Alberta, a Canada Corporation

j TITLE OF INVENTION: UNIVERICANT THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

FILE REFERENCE: 07.254/049002

CURRENT APPLICATION NUMBER: US/09/733,524

CURRENT PILING DATE: 1999-06-05

PRIOR FILING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PARLER PARLER ARESEQ for Windows Version 4.0

SOFTWARE: PARLER

TYPE: PRT
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                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: H. pylori strain 802 PutA fucosyltransferase
US-10-764-212-18
                                                                                                                                                                                                                                                                          Length 440;
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                 CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 18
LENGTH: 440
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                                                                                                                                                 TYPE: PRT
ORGANISM: Helicobacter pylori
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61 NEPSDLVPGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYLRMP 120
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241 YGYVTEKIIDAYFSHTIPIYMGSPSVAKDFNPKSFVNNHDFKNFDEAIDYVRYLHTHPNA 300
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                                                                                                       1 MFQPLLDAFIESASIKKMPLSYPPLKIAVANWWGGAEEFKKSAMYFILSQRYTITLHQNP
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                                                  Gaps
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APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REPERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT RILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR PILING DATE: BARLIER FILING DATE: 1998-06-05
PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PastSEQ for Windows Version 3.0
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  Length 440;
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99.4%; Score 2347; DB 3;
99.5%; Pred. No. 7.8e-191;
tive 0; Mismatches 2;
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83.0%; Pred. No. 1.3e-162;
iive 34; Mismatches 26;
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; Sequence 8, Application US/10392098
; Publication No. US20030166212A1
; GENERAL INFORMATION:
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; ORGANISM: Helicobacter pylori
US-10-392-098-8
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Matches 377; Conservative
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                                                                                  61 RNPDKPADIVFGNPLGSARKILSYQNTKRIFYTGENESPNFNLFDYALGFDELDFRDRYL
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; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALBHA-1, 3-FUCOSYLTRANFERASE
; FILE REFERENCE: 07254/04901
; CURRENT APPLICATION NUMBER: US/10/189,977
; CURRENT PILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/99/092,315
; PRIOR PILING DATE: 1998-06-05
; PRIOR PILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NOS: 22
; SEQ ID NOS: 22
; SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 PLLELSQNTSFKIYRKIYQKSLPLLRVIRRWVKK 454
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; ORGANISM: Helicobacter pylori
US-10-189-977-8
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/733,524A
FRIOR PILING DATE: 2000-12-07
FRIOR APPLICATION NUMBER: US 60/092,315
FRIOR PILING DATE: 1998-06-05
FRIOR PILING DATE: 1998-06-06
FRIOR FILING DATE: 1997-06-06
SPRIOR FILING DATE: 1998-06-05
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238 SQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTH
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Sequence 18, Application US/09733524

Patent No. US20020068347A1

GENERAL INPORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhonguning

TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION NUMBER: US/09/733,524

CURRENT APPLICATION NUMBER: 09/092,315

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0
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84.9%; Score 2006.5; DB 3; Length
Best Local Similarity 82.6%; Pred. No. 7.5e-162;
Matches 375; Conservative 35; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: helicobacter pylori fucosyltransferase
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 11637 from NCTC11637
US-09-733-524-18
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Publication No. US20020164749A1
US-09-733-524-18
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US-10-120-319-2
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       APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT FILING DATE: 2002-04-09
FRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/092,315
FRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/048,857
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-06-06
FRIOR PILING DATE: BARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTESE for Windows Version 3.0
SSOFTWARE: FASTESE for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                          28; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                         Query Match 84.6%; Score 1999; DB 4; Length 486; Best Local Similarity 77.6%; Pred. No. 3.6e-161; Matches 377; Conservative 35; Mismatches 28; Indels 4
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; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
; PRIOR FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-2
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IKKLGL 486
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GENERAL INFORMATION:
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US-10-189-977-2
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EVCOSITARANSERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: UNABER: US/10/392,098
CURRENT APPLICATION NUMBER: US/09/733,524A
PRIOR PILING DATE: 1009/133,524A
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 2
SEQ ID NO 2
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Best Local Similarity 77.6%; Pred. No. 3.6e-161;
Matches 377; Conservative 35; Mismatches 28;
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 486
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                                                                                                                                                        ; ORGANISM: Helicobacter pylori
US-10-189-977-2
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Matches 377; Conservative
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US-10-764-212-2
                                                                                    Query Match
84.6%; Score 1999; DB 4; Length 486;
Best Local Similarity 77.6%; Pred. No. 3.6e-161;
Matches 377; Conservative 35; Mismatches 28; Indels 4
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| Sequence 2, Application US/10764212
| Publication No. US20050164338A1
| GENERAL INFORMATION:
| APPLICANT: Simala-Grant, Joanne | APPLICANT: Taylor, Diane | APPLICANT: Dohnson, Karl F. APPLICANT: Bezila, Daniel James | APPLICANT: Governors of the University of Alberta | APPLICANT: Governors of the University of Alberta | TITLE OF INVENTION: H. Pylori Pucosyltransferases | TITLE OF INVENTION: H. Pylori Pucosyltransferases | TITLE OF INVENTION: H. Pylori Pucosyltransferases | TITLE OF INVENTION: H. Pylori Pucosyltransferases | CURRENT APPLICATION NUMBER: US/10/764,212 | CURRENT FILING DATE: 2004-01-22 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NO S: B1 | LENGTH: 486
                  ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-392-098-2
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ORGANISM: Helicobacter pylori
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481 IKKLGL 486
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Best Local Similarity
LENGTH: 486
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane B.

APPLICANT: Taylor, Diane B.

APPLICANT: Ge, Zhonganing

TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: UNDER: US/09/733,524

CURRENT APPLICATION NUMBER: US/09/733,524

FRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2
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  28; Indels
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  35; Mismatches
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; OTHER INFORMATION: Strain 1182 from UA1182
US-09-733-524-2
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Matches 377;
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US-10-953-349-5128
Sequence 5128, Application US/10953349
; Publication No. US20060107345A1
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1771.230 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/USI1_NEW_PUB.pep:*
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2362
1 MPQPLLDAPIESASIKKMPL......YHKSLPLLRAIRRWVKKLGL 440
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-953-349-5128

US-10-959-349-5128

US-10-449-902-44967

US-11-197-712-284

US-10-449-902-52598

US-10-537-642-18

US-10-537-642-18

US-11-293-697-4748

US-11-293-697-4748

US-11-375-551-20

US-11-070-573-68

US-11-070-573-68

US-11-070-573-68

US-10-527-411-153

US-10-527-411-153

US-10-527-411-153

US-10-527-411-153

US-10-527-411-153

US-10-527-411-153

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US-10-527-411-163

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Listing first 45 summaries
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Match Length
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513
954
1791
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5. 4.6         873         6         US-10-527-411-159         Sequence 169, App           5. 5         4.6         1127         6         US-10-527-411-40         Sequence 40, App           6. 5         4.6         1129         6         US-10-527-411-40         Sequence 40, App           6. 6         1129         6         US-10-527-411-40         Sequence 40, App           6. 8         4.6         1130         6         US-10-527-411-40         Sequence 41, App           6. 8         4.6         1130         6         US-10-527-411-34         Sequence 13, App           7. 5         4.6         1737         7         US-10-527-411-34         Sequence 13, App           7. 5         4.6         US-10-527-411-39         Sequence 13, App           7. 7         4.0         US-10-527-411-40         Sequence 30, App           7. 7         4.5         876         6         US-10-527-411-6         Sequence 66, App           7. 7         4.5         876         6         US-10-527-411-6         Sequence 67, App           7. 7         4.5         876         6         US-10-527-411-6         Sequence 67, App           7. 7         4.5         879         6         US-10-527-411-6	ALIGNMENTS  SULT 1  -10-953-349-5129 Sequence 5129, Application US/10953349 Publication No. US20060107345A1 Publication No. US20060107345A1 APPLICANT: ALEXANDROV, Nickolai et al. TITLE OF INVENTION: ENCONDED THERBY FILLE OF INVENTION: ENCONDED THERBY FILLE OF INVENTION: ENCONDED THERBY FILLE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT APPLICATION NUMBER: US/10/953,349	h. 6.7%; Score 159; DB 6; Length 302; Similarity 25.1%; Pred. No. 1.5e-05; 70; Conservative 45; Mismatches 94; Indels 70; Gaps 12;	6 KRGFASFVASNFNAPKRNAFYDALNSIEPVTGGSVKNTLGYKVGNKNEFLSQYK 230	1 FNLCFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAI 288 	9 DYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFK 333 ::   :	4 TILENDTIYHNNPFVFYRDLNEPLVSIDDLRADYNNLRAD 373   :
109.5 109.5 109.5 109.5 100.5 107.5 107.5 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1 107.1	RESULT 1 US-10-953-349-5129 Sequence 5129, A Publication No. GENERAL INFORMAT APPLICANT: ALEX TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT FILE REFERENCE: CURRENT APPLICAN CURRENT FILING NUMBER OF SEQ I SOFTWARE: PATEN LENGTH: 302 TYPE: PATEN LENGTH: 302 TYPE: PATEN LENGTH: 302 TYPE: PATEN CORGANISM: Arab	atch cal		231	289	334
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APPLICANT: Bougneleret, Lydie
APPLICANT: Bougneleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: PULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REPERENCE: 78.1054.CIP
CURRENT APPLICATION NUMBER: US/11/197,712
CURRENT PILING DATE: 2005-08-04
PRIOR APPLICATION NUMBER: US/09/876,997
PRIOR PLING DATE: 2001-06-08
PRIOR PLING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-07
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                                                    ----NDIIYHNNPFVFYRDLNEPLVSIDDLRADYNNLRAD 373
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APPLICANT: National Institute of Parobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Poundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERENCE: MOA-A020251-US
CURRENT APPLICATION NUMBER: UP 2002-203269
PRIOR FILING DATE: 2003-05-29
PRIOR PLILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR PLILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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                                                                                                                                                                                  264 ESAVLAKPKSLKHRAVWKKERPGNLKGDKELKIHRIYPL 302
                                                                                                                                                     374 YNNLRADYNNLRADY-----NNLRADYDRLLQNRSPL 405
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Publication No. US20060130160A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
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; ORGANISM: Oryza sativa
US-10-449-902-44967
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LENGTH: 246
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                          APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 TRVREQEEESPNFKKRPCKCSRGGSDTVYH----VPVRERGRFEMESVFLRGKSVTQEAL 248
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.7%; Score 159; DB 6; Length 323; Best Local Similarity 25.1%; Pred. No. 1.7e-05; Matches 70; Conservative 45; Mismatches 94; Indels '
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana
US-10-953-349-5127
                                                                                                                                                                                                                                                                                                          ; ORGANISM: Arabidopsis thaliana US-10-953-349-5128
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          SENERAL INFORMATION:
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US-10-953-349-5127
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LENGTH: 323
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SOFTWARE: PatentIn version 3.2
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Matches 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 TITLHQNPNEPSDLVFGSPIGAARKIL------SYQNTKRVFYAGENEVPNF 98
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Fublication No. US2006123505A1
GENERAL INPORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGHT PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
FILE REFERENCE: MOA-A0205Y1-US
FILE REFERENCE: 2003-05-29
PRIOR PRLING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-338870
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52598
LENGTH: 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LDAFIESASI-----KKMPL-SYPPLKIAVANWW------GGAEEFKKSAMYFILSQRY
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                                                                                                                                                                                                                                                                                                           Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 VAKDFNP--KSFVNVHDFKNPDEAIDYVRYLHTHPNAYLDMLYE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86; Indels
                                                                                                                                                                                                                                                                                                       6.0%; Score 141; DB 7; Length 40
22.7%; Pred. No. 0.00073;
tive 51; Mismatches 119; Indels
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PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 284
LENGTH: 406
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 22.79
Matches 78; Conservative
                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Oryza sativa
US-10-449-902-52598
                                                                                                                                                                                                                        ; NAME/KEY: SIGNAL
; LOCATION: -31...1
US-11-197-712-284
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252
188 YKIVMTTSLSSDVPVGYFSWAEYDIMAPV----PPKTEEALAAAFISNCGARNFRLQAL 242
                                                                               256 TIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEA---IDYVRYLHTHPNAYLDML---YENP 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 TGGGSVKNTLGY----KVGNKNEPLSQYKFNLCFENSQGYGYVTEKIIDAY-----
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TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF PILE REPREDICE: PPI-103X
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
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APPLICANT: Epimmune, Inc.
APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Doolan, Denise L.
APPLICANT: Stancci, Daniel J.
APPLICANT: Sidney, John
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PRIOR FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                            310 LNTLDGKAYFYQDLSFKKILD 330
                                                                                                                                                                                                                                                                                                                               360 SD------SFKALID 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8, Application US/10537642; Publication No. US20060165719A1; GENERAL INFORMATION:
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Sequence 6, Application US/10537642 Publication No. US20060165719A1 GENERAL INFORMATION:
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US-11-293-697-4748
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Matches 86; Conserv
                                                                                                                                                                                                                                                                     SEQ ID NO 4748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 EVPNFNLFD---YAIG-FDELDLRDRYLRMPLYYDRLHHKAESVNDTT--APYKIKPDSL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 YTLKKP-----SHHFKEKHPHLCAVVNDB----SDPLKRGFASFVASNPNAPKR----- 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 KDFNPKSFVNVHD-PKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KILDFFKTILENDTI-----YHNNPFVFYRDLNEPLVSIDDLRADYNNLRADY- 374
                                                                                                                                                                                           APPLICANT: The United States of America as Represented by the APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Settler, Alessandro APPLICANT: Settler, Doolan, Denise L. APPLICANT: State, Doolan, Denise L. APPLICANT: State, Doolan, Denise L. APPLICANT: State, Denise J. APPLICANT: State, Denise J. APPLICANT: Southwood, Scott APPLICANT: Southwood, Scott TILLE REFRENCE: EPI-103X
TITLE REFRENCE: EPI-103X
TITLE OF INVENTION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
FRIOR APPLICATION NUMBER: US 60/431,494
FRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9%; Score 115; DB 6; Length 1791;
18.6%; Pred. No. 0.9;
tive 80; Mismatches 156; Indels 170;
                                                                                                                     Sequence 18, Application US/10537642 Publication No. US20060165719A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1347 NYDKKL-----LKKL 1356
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ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Conservative
                                                                                                                                                                                APPLICANT: Epimmune, Inc
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Matches 93; Conserv
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412 -PFHK 415
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145 DSLYTLKKPSHHFKEKHPHLCAVVNDESDPLKRGFASFVASNPN-APKRNAFYDALNSIE 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 KORFLSQYKFNLCFENSQGYGYVTEKI-IDAYFSHTIPIYWGSPS---VAKDFNPKSFVN 277
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APPLICANT: The United States of America as Represented by the
APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Daniel J.
APPLICANT: Carucci, Daniel J.
APPLICANT: Sidney, John Parise L.
APPLICANT: Sidney, John Parise L.
APPLICANT: Sidney, John Parise L.
APPLICANT: Southwood, Scott
TITIE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
TITIE REFERENCE: EPI-103X
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT APPLICATION NUMBER: US 60/431,494
PRIOR APPLICATION NUMBER: US 60/431,494
NUMBER OF SEQ ID NOS: 1161
SEOFFWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.8%; Score 113.5; DB 7; Best Local Similarity 26.8%; Pred. No. 0.11; Matches 55; Conservative 30; Mismatches 77;
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18.9%; Pred. No. 0.68;
tive 48; Mismatches 128;
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Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT PILICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PARENTIN Ver. 2.1
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1778 -----GPLNVSIATGY------SAPMDFNSASALYYWELFYYTPMMCFQRL 1817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 YNNLR------ADYNNLRADY-----NNLRA-----DYNNLRADY 395
---KHPHLCAVVNDESD-----PLKRGFASFVASNPNAPKRNA 194
                                                                                                                                                                                  234 CFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKS--------FVNV 278
                                                                                                                                                                                                                                                                                                                                                                    318 ---YFYODLSFKKILDFFKTILENDTIYHNNPFVFYRD-LNE-----PLVSIDDLRAD 366
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OTHER INFORMATION: Amino acid sequence of the 8836 "BCA" triple fusion protein in OTHER INFORMATION: encoded by SEQ ID NO:67 US-11-070-573-68
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----DILFLRETHSGAQY 1612
                                                                                                             1733 TYDNTWESAFPYFDETKQQFVLINDADHDSGMTQQGIVKNIKKYK------- 1777
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                                                                                                                                                                        157 FKE------KHPHLCAVVNDESD-----PLKRGFASFVASNPNAPKRNA 194
                                                                                                                                                                                                                                                                         195 FYD------ALNSIE---PVTGGGSVKNTLGYKVGNKNEFLSQYKFNL 233
                                                                          117 LRMPLYYDRLH------HKAESVNDT--TAPYKIKPD-----SLYTLKK--PSHH 156
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APPLICANT: Meade, Thomas
APPLICANT: Meade, Thomas
APPLICANT: Mond, Haley
APPLICANT: Mond, Haley
APPLICANT: Sheets, Joel
APPLICANT: Sheets, Joel
APPLICANT: Merlo, Donald
APPLICANT: Merlo, Donald
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Insecticidal Toxin Complex Fusion Proteins
FILE REFERENCE: DAS-118XC1
FILE REFERENCE: DAS-118XC1
FILE REFERENCE: DAS-118XC1
FILE REFERENCE: DAS-118XC1
FRIOR APPLICATION NUMBER: 60/549,502
FRIOR APPLICATION NUMBER: 60/549,516
FRIOR APPLICATION NUMBER: 60/549,516
FRIOR PILING DATE: 2004-03-02
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
LENGTH: 5001
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4.7%; Score 111.5; DB 7; Length 5001;
Best Local Similarity 19.6%; Pred. No. 7.8;
Matches 113; Conservative 60; Mismatches 158; Indels 245;
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Sequence 68, Application US/11070573 Publication No. US20060168683A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Cai, Charles
APPLICANT: Meade, Thomas
APPLICANT: Moon, Haley
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APPLICANT: Meade, Thomas
APPLICANT: Moon, Haley
APPLICANT: Burton, Stephanie
APPLICANT: Sheets, Joel
APPLICANT: Sheets, Joel
APPLICANT: Mosley, Aaron
TITLE OF INVENTION: Insecticidal Toxin Complex Fusion Proteins
FILE REPERENCE: DAS-118XC1
CURRENT FILING DAFE: 2006-03-02
PRIOR PPLICATION NUMBER: 60/549,502
PRIOR APPLICATION NUMBER: 60/549,516
PRIOR APPLICATION NUMBER: 60/549,516
PRIOR PILING DAFE: 2004-03-02
PRIOR PILING DAFE: 2004-03-02
PRIOR PILING DAFE: 2004-03-02
PRIOR FILING DAFE: 2004-03-02
PRIOR FILING DAFE: 2004-03-02
PRIOR FILING DAFE: 2004-03-02
PRIOR FILING BAFE: 2004-03-02
NUMBER: OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60
: LENGTH: 4995
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US-11-070-573-60
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Publication No. US20060168683A1
GENERAL INFORMATION:
APPLICANT: Hey, Timochy
APPLICANT: Cai, Charles
APPLICANT: Madde, Thomas
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ORGANISM: Artificial Sequence
                                                                                                        157 FKB-----
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                                                             P-----GSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRD-----RY 116
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APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
APPLICANT: Carucci, Daniel J.
APPLICANT: Carucci, Daniel J.
APPLICANT: Sidney, John PALIFORM: Sidney, John PAPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REPERENCE: BFI-103X
CURRENT PAPLICATION NUMBER: US/10/537,642
CURRENT APPLICATION NUMBER: US 60/431,494
PRIOR FILING DATE: 2002-12-06
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Publication No. US20060165719A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1161
SOFTWARE: PatentIn version 3.2
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99 NLFDYAIGFDELDLRDRYLRMPLYYDRLHHKAESVNDTTAPYKIKPDSLYTLKKPSHHFK 158

98;

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---- VNTNILY----- 618
                                                       EKHPHLCAVVNDESDPLKRGFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYK 218
                                                                                       219 VGNKNEFLSQYKFNLCFENSQGYGY-----VTEKIIDAYFSHTIPIYWGSPSVAKDFN 271
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                                                                                                                                                                                                                                                                                                                                                                                               325 FKKILDFFKTILENDTIYHNNPFV------FYRDLNEPLVSIDDLRADYNNLR 371
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  584 NIFNNMNHLNHLD-NHSYIQNNLYKNHMN---
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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 protein search, using sw model OM protein August 11, 2006, 19:30:38; Search time 120.286 Seconds (without alignments) 1733.289 Million cell updates/sec Run on:

US-10-764-212-20

Title: Perfect

2458 1 MFQPLLIDAFIDSTHLDETTH.....TSFKIYRKAYQKSLPLLRAI score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_8:\* Database

geneseq1980s:\* geneseqp190s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003s:\* geneseqp2003s:\* geneseqp2003s:\* geneseqp2005s:\* geneseqp2006s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aeb70149 Helicobac	Aaw86008 Helicobac	Ħ.	Ħ.		Hel			Adj77810 Helicobac	Adj27345 Alpha-1,3	Aeb70131 Helicobac	Abg30887 H. pylori	H	Adj77812 Helicobac	Adj27347 Alpha-1,3		Aeb70145 Helicobac				Adj27355 Alpha-1,3		Aeb70195 H. pylori
ID	AEB70149	AAW86008	ABG30884	ABG30881	ABG3 0886	ADJ77814	ADJ27349	AEB70135	ADJ77810	ADJ27345	AEB70131	ABG30887	ABG3 0882	ADJ77812	ADJ27347	AEB70133	AEB70145	AEB70147	ABG30883	ADJ77820	ADJ27355	AEB70141	AEB70195
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Abg30885 H. pylori	Abu52257 Helicobac	Aeb70197 H. pylori	Adj77816 Helicobac	Adj27351 Alpha-1,3		He	Ħ.	Ħ.	Aeb70205 H. pylori	H.	Ξ.	Aeb70204 H. pylori	Aeb70203 H. pylori		Aeb70193 H. pylori	Aeb70212 Helicobac	Abu51151 Helicobac	Abu51720 Helicobac	Aeb70190 H. pylori	Abu51509 Helicobac	Abu51153 Helicobac
ABG30885	ABU52257	AEB70197	ADJ77816	ADJ27351	AEB70137	AEB70211	AEB70154	AEB70199	AEB70205	AEB70201	AEB70202	AEB70204	AEB70203	AEB70206	AEB70193	AEB70212	ABU51151	ABU51720	AEB70190	ABUS1509	ABU51153
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69.3	68.4	66.7	49.6	49.6	49.6	47.4	45.9	45.9	43.8	41.3	40.7	40.7	40.5	40.4	39.5	35.2	24.9	21.7	21.7	18.5	17.4
1702.5	1681	1639	1218	1218	1218	1164	1129	1129	1075.5	1015.5	1001.5	1000	966	993	972	864.5	611.5	534.5	532.5	454.5	426.5
24	25	79	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucosos residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein. New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids. Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 20. Bezila DJ; Fucosyltransferase; protein production; enzyme Johnson KF, Claim 2; SEQ ID NO 20; 97pp; English. AEB70149 standard; protein; 456 AA. Helicobacter pylori; strain 948. (NEOS-) NEOSE TECHNOLOGIES INC. (UYAL-) UNIV ALBERTA. 22-JAN-2004; 2004US-00764212. 22-JAN-2004; 2004US-00764212. Simala-Grant J, Taylor D, (first entry) WPI; 2005-521417/53. N-PSDB; AEB70148 US2005164338-A1. 06-OCT-2005 28-JUL-2005 AEB70149; AEB70149 

Sequence 456 AA; Query Match

Length 456; DB 9; 100.0%; Score 2458;

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                                                                               61 SNPNBFSSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYL 120
                                                                                                                                                                                                       241 GYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQN 300
                                                                                                                                                                                                                                                                          LVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRRDH 420
                                                                                                                                                                                                                                                                                     LVSVDDIEREDHDDIERWYDDLEWYYDDLEWYNYDDLEWYNYDDLERWYNYDDLERDHDDLERDH 420
                               9
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                                                                                                                       121 RMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGF
                                                                                                                                                               181 ASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTIGYKVKNKNEFLSQYKFNLCFENSQ
                                                                                                                                                                                                                                  301 AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNEP
                                                                                                                                                                                                                                            61 SNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYL
                                                                                                              RMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCAL I HNESDPWKRGF
                                                                                                                                                    ASFVASNPNAPIRNAFYDALNAIEPVASGGSVRNTLGYKVKNKNEFLSQYKFNLCFENSQ
                                                                                                                                                                                           GYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQN
                               1 MPQPLLDAPIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILH
                                                 1 MPQPLLDAFIDSTHLDETTHKPPLNVALANWWPLKNSEKKGPRDFILHFILKQRYKIILH
          Gaps
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-1,3-fucosyltransferase; fucT gene; Lewis X; Lewis Y; sialyl Lewis X; tumour associated antigen; cancer; infection; mucosal disease; diagnosis; fucosylated oligosaccharide.
           Indels
                                                                                                                                                                                                                                                                                                                  ERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI 456
 100.0%; Pred. No. 2.7e-202; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori alpha-1,3-fucosyltransferase.
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/note= "Asn is N-glycosylated"
137. .139
/note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
341. .343
/note= "Asn is N-glycosylated"
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378. .384

385. .391

/note= "peptide repeat"

/note= "peptide repeat"

/note= "peptide repeat"

/note= "peptide repeat"

/note= "peptide repeat"
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/note= "peptide repeat"
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Best Local Similarity 100. Matches 456; Conservative
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This is the amino acid sequence of the novel alpha-1,3-
fucosyltransferase of Helicobacter pylori NGTC 11639, as deduced from the
newly isolated fucT gene (see AAV80321). The enzyme is characterised by 8
c-terminal heptad repeats and by the lack of a transmembrane domain. The
absence of a transmembrane domain allows the enzyme to be readily
released from recombinant host cells. The enzyme can be used in the
production of fucosylated oligosaccharides such as Lewis X, Lewis Y and
sialyl Lewis X, which are structurally similar to certain tumour
associated antigens found in mammals. These glycoconjugates also have
mammalian tumours. The enzyme can also be used to raise specific
antibodies. Inhibition of abnormal fucT gene product activity can be used
for the treatment of innestinal mucosal disease. (Updated on 17-OCT-2003
to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 ENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated alpha-1-3-fucosyltransferase gene - obtained from
Helicobacter pylori, used to develop products for the diagnosis and
treatment of intestinal mucosal diseases, e.g. tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.5%; Score 1929.5; DB 2; Length 464; 79.1%; Pred. No. 7.3e-157; ative 41; Mismatches 46; Indels 9;
                                                                                                                     435. .437
/note= "Asn is N-glycosylated"
                    406. .412
/note= "peptide repeat"
note= "peptide repeat"
                                                                      413. .419
/note= "peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Fig 2; 51pp; English.
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Matches 364; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (UYAL-) UNIV ALBERTA
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                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                      06-JUN-1997;
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                                                                      Peptide
                          Peptide
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fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple helix sequences and for alphal, 3-fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or call are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alphal, fucosyltransferase encdoed by the fucT gene. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 476 AA;

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The invention relates a purified transmembrane segment-free alpha 1,3-
fucosyltransferase polypeptide, having a repeat of the sequence: X_1-X_2-
Leu-Argy, A=X 4-Tyr, where X:1, X=2 and X 4 is a Asp or Asn; and X=1 is

[11e, Val or Ala. Also included are the nucleic acid encoding the protein

(including its complement or fragment), a vector containing the nucleic

acid, a host cell containing nucleic acid or vector, an antibody which

selectively binds to the protein and a gene expression system for

comprising a host cell modified with the nucleic acid or its

comprising a host cell modified with the nucleic acid or its

comprising thost cell modified with the nucleic acid or its

comprising the protein with a substrate such as LackAc-R and GDP-fucose,

contacting the protein with a substrate, to produce oligosaccharides

contacting the protein with a substrate, to produce oligosaccharides

and purifying the host cell with a substrate, to produce oligosaccharides

and purifying the obtained oligosaccharides. The nucleic acid is useful

contacting the nucleic acid using polymerase claid, by contacting a sample with a

cucleic acid probe that hybridissation of the probe; or by

polynucleotide, and detecting hybridisation of the probe; or by

tucosyltransferase-fusion protein, by growing the host cell containing a

cucro operably linked to a polynucleotide encoding a desired polypeptide

cor peptide under conditions which allow expression and secretion of the

cup protein and isolating the fusion protein. The antibody is useful

cor peptide under conditions which allow expression and secretion of the

cor peptide under conditions which allow expression and secretion of the

cor peptide under conditions which allow expression and secretion of the

cor peptide under conditions which allow expression and secretion of the

cor peptide under conditions which allow bresence of the protein in the

sample is indicative of infection by Halloobacter pylori or the presence

of malignant cells. The antibody is also useful for
416
                    LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzyme; fucT; alphal, 3 fucosyltransferase; oligosaccharide; Lex; Ley; slex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                               H. pylori alphal, 3 fucosyltransferase #4.
                                                                                                                                                                                                                                                  ABG30884 standard; protein; 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori; strain 26695A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 6; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2000; 2000US-00733524.
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(first entry)
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21-OCT-2002
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                                                                                28
                                                                                                                        FENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKOFNPKSFVNVHDFNNFDEAIDYIKYL
                                                                                                                                                                                                                                                                                                                                         58 ILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENBVPNFNLFDYAIGFDELDFND
                                                                                                                                                               118 RYLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDP
                                                                                                                                                                                                                                HAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR
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                                                    1 MPQPLLDAFIDSTHLDETTHK----PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKI
                                                                                                                                                                                                                   176 WKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLC
                                                                                                                                                                                                                                                                                                                                                                              ---DDLRRDHDDLRVNYDDLRVNYDDLRVNYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bnzyme, fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley;
sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                           24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
Query Match 78.5%; Score 1929; DB 5; Best Local Similarity 77.5%; Pred. No. 8.3e-157; Matches 368; Conservative 39; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG30881 standard; protein; 501 AA
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Misc-difference 272
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The invention relates a purified transmembrane segment-free alpha 1,3the constraint fransferase polyapetide, having a repeat of the sequence: X 1-X 2teu-Arg-Xx 3-X 4-Tyr, where X 1, X 2 and X 4 is App or Abn; and X 3 is

Iteu-Arg-Xx 3-X 4-Tyr, where X 1, X 2 and X 4 is App or Abn; and X 3 is

Iteu-Arg-Xx 3-X 4-Tyr, where X 1, X 2 and X 4 is App or Abn; and X 3 is

Iteu-Arg-Xx 3-X 4-Tyr, where X 1, X 2 and X 4 is App or Abn; and X 3 is

Ite, Val or Ala. Also included are the mucleic acid encoding the protein

C (including its complement or fragment), a vector containing the mucleic acid or vector, an antibody which

selectively binds to the protein and a gene expression system for

comprising a host cell modified with the mucleic acid or its

comprising a host cell with a substrate, to produce oligosaccharides, by contacting the protein with a substrate, to produce oligosaccharides, or by culturing the cell, or contacting the protein with a substrate, to produce oligosaccharides and purifying the obtained oligosaccharides. The nucleic acid is useful

c and purifying the obtained oligosaccharides. The nucleic acid is useful

c contacting the bost cell with a substrate, to produce oligosaccharides

and purifying the obtained oligosaccharides. The nucleic acid is useful

c contacting the bost cell with a substrate, to produce oligosaccharides

and purifying the nucleic acid using polymerase chain reaction (PCR). The

c mullifying the nucleic acid using polymerase chain reaction (PCR) amplifying the nucleic acid using polymerase chain reaction (PCR) and protein and isolating the fusion protein. The probe; or the protein in the customent of the protein in the ample. The presence of the protein in the and protein and isolating the fusion protein. The metabody is useful

c for detecting the protein in a sample The presence of the protein in the and and and an and an and an and an and an and an and an and an and an and an and an and an and an and an analy and an analy and an analy and an analy and an analy and an an 465. .501 /note= "Region not encoded by sequence appearing as ABK89249" segment-free alphal, 3-fucosyltransferase producing fucosylated oligosaccharides. 'note= "Encoded by AT" /note= "Encoded by GT' 6; Fig 2A; 37pp; English 98US-00092315. 07-DEC-2000; 2000US-00733524 Purified transmembrane polypeptide useful for UYAL-) UNIV ALBERTA WPI; 2002-582480/62. Misc-difference 278 Ge Z; N-PSDB; ABK89249 Sequence 501 AA; US2002068347-A1 35-JUN-1998; 06-JUN-2002 Taylor DE,

4 9; Gaps DB 5; Length 501; Query Match 78.2%; Score 1921.5; DB 5; Length Best Local Similarity 79.1%; Pred. No. 3.9e-156; Matches 364; Conservative 41; Mismatches 46; Indels 1 MFQPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII 58 

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The invention relates a purified transmembrane segment-free alpha 1,3-fucosyltransferase polypeptide, having a repeat of the sequence: X\_1-X\_2-Leu-Arg-X\_3-X\_4-Tyr, where X\_1, X\_2 and X\_4 is Asp or Asn; and X\_3 is 1le, Val or Ala. Also included are the nucleic acid encoding the protein 356 416 59 LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR 118 236 296 298 (including its complement or fragment), a vector containing the nucleic acid, a host cell containing nucleic acid or vector, an antibody which selectively binds to the protein and a gene expression system for producing transmembrane segment-free alphal, 3- fucosyltransferase, comprising a host cell modified with the nucleic acid or its 119 YLRMPLYYAYLHYKAMLVNDTTSPYKLK --ALYTLKKPSHKFKENHPNLCALIHNESDPW 297 AHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRD Enzyme, fucT, alphal, 3 fucosyltransferase; oligosaccharide; Lex; Ley; sLex; Helicobacter pylori infection; malignant cell; mammalian tumour. 177 KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF ENSQGYGYVTEKILDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDL Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides. 456 417 RRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI H. pylori alphal, 3 fucosyltransferase #6. ABG30886 standard; protein; 479 AA Example 3; Fig 6; 37pp; English. Helicobacter pylori; strain 763. 07-DEC-2000; 2000US-00733524. 98US-00092315 (revised)
(first entry) (UYAL-) UNIV ALBERTA WPI; 2002-582480/62. Ge Z; JS2002068347-A1. 05-JUN-1998; 29-AUG-2003 21-OCT-2002 raylor DE, ABG30886; 237 357 ABG30886 RESULT 셤 ઠે g 쇰 셤 셤 8 셤 ð 셤 8 ð ò

contacting the protein with a substrate such as Lexy, Ley or slex, by contacting the protein with a substrate such as LackNo-R and GDP-fucose, and purifying the protein with a substrate such as LackNo-R and GDP-fucose, contacting the host cell with a substrate, to produce oligosaccharides and purifying the host cell with a substrate, to produce oligosaccharides are a probe for detecting the mucleic acid, by contacting a sample with a mucleic acid probe for detecting the mucleic acid, by contacting a sample with a mucleic acid probe that hybridisation of the probe; or by contacting a maniferance contains a maplifying the mucleic acid using polymerase chain reaction (PCR). The host cell is useful for producing a transmembrane segment-free alphal, 3-thosy cell is useful for producing a transmembrane segment-free alphal, 3-thosy cell is useful for producing a transmembrane segment-free alphal, 3-thosy cell is useful as sample and isolating the fusion protein. The antibody is useful for detecting the protein in a sample. The presence of the protein in the sample is indicative of infection by Helicobacter pylori or the presence of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alphal, 3-thosy, me and/or triple helix sequences and for alphal, 3-thosy cell is necessarie sequence and for alphal, 3-the protein or cell are useful in the development of assays to detect the protein or cell are useful in the development of assays to detect the protein or alphal, 3-the protein or cell are useful in the development of assays to detect the protein or cell are useful in the development of assays to detect the protein or the presence of the protein or cell are useful in the development of assays to detect the protein or the presence of the protein or cell are useful sequences. mammalian tumours. The present sequence represents an H. pylori alphal, 3 fucosyltransferase encdoed by the fucT gene. (Updated on 29-AUG-2003 to standardise OS field) enzymatically active portion. The protein and cells are useful for 8888888888888888888888888888888888

Sequence 479 AA;

ġ 415 LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPN-FNLFDYAIGFDELDFND 117 118 235 238 298 FENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDBAIDYIRYL 295 HAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR 355 401 1 MFQPLLDAYVESASIEKMAKSKPPPLKIAVANWW--GDEEIKEFKNSVLYFILSQRYTIT 58 LKRGFASFVASNDNAPIRNAFYDALNSIBPVTGGGSVRNTLGYNVKNKNEFTSQYKFNLC RYLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDP WKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLC HIHKNAYLDMLYENPLATLDGKAYFYQNLSFKKILAFFKTILENDTIYHDNPFIFC---R MPOPLLDAFIDSTHLDE--TTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKORYKII DINEPLUSY-------DDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD 24; Gaps LRVNYDDLRRDHDDLRRDHERLLSKATPLLELSQNTSPKIYRKAYQKSLPLLRAI 456 77.2%; Score 1897; DB 5; Length 479; 76.4%; Pred. No. 4.7e-154; ive 42; Mismatches 46; Indels 2 76.48; Matches 363; Conservative Best Local Similarity 59 59 176 118 119 179 236 962 299 356 402 Query Match ઠે 셤 ሯ 셤 g Š 셤 a 8 셤 ò 셤 ઠે ઠે 셤 ò

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ADJ77814 standard; protein; 485 AA.

ADJ77814 RESULT

(first entry)

06-MAY-2004 ADJ77814;

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Futh and FutB) of Helicobacter pylori (H. pylori). Specifically, it referse to alpha 1-3/4 fucosyltransferase enzymes (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it referse to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expression systems. This polypeptide sequence is an H. pylori strain 1218 FutB protein sequence of the invention. This invention relates to novel isolated polynucleotides and the encoded New isolated polynucleotide encoding fucosyltransferase protein, usefu for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids. 1 MFQPLLDAYIESASIEKITSKSPPPLKIAVANWW--GDEEVEFKKNILYFILSQHYTIT 119 YLRMPLYYDRIHHKAESVNDTTSPYKLKDDSLYALKKPSHHFKENHPNLCAVVNNESDPL 239 ENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLH LHSNPNEBSDLVPGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR 119 YLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPW 297 AHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRD 1 MFQPLLDAFIDSTHLDBTTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII KRGFASFVASNPNAPIRNAFYDALNAI EPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF ENSOGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; 30; Length 485; 47; Indels fucose; N-acetylglucosamine; glycoconjugate; enzyme. Helicobacter pylori strain 1218 FutB protein SeqID Duery Match 77.2%; Score 1897; DB 8; Best Local Similarity 75.4%; Pred. No. 4.8e-154; Matches 362; Conservative 41; Mismatches 47; Claim 16; SEQ ID NO 6; 72pp; English (NEOS-) NEOSE TECHNOLOGIES INC. 08-NOV-2002; 2002US-0424894P. 23-JUL-2003; 2003WO-US023057. 23-JUL-2002; 2002US-0398156P. Johnson KF, Bezila DJ; Helicobacter pylori WPI; 2004-123401/12 N-PSDB; ADJ77813 Sequence 485 AA; WO2004009838-A2 29-JAN-2004. 29 177 237 Query Match ð 셤 ઠ

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296 298 356 355 406 415 455 475

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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
119 YLRMPLYYDRLHHKAESVNDTTSPYKLKPDSLYALKKPSHHFKENHPNLCAVVNNESDPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                              299 THPNAYLDMLYENPINTLDGKAYFYQNLSFKKILDFFKTILENDTIYHDNPPIF---YRD
                                                                                                                                                                                                                                                                                          LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNY------
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                                                                                                                                                                                                           297 AHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRD
                                                                                                                                                                                                                                                                                                                                                                               -----DDLRRDHDDLRRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRA
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                                         KRGFAS FVASNPNAPIRNAFYDALNAI BPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF
                                                                                                                           ENSOGYGYVTEKI LDAYFSHTI PI YWGSPSVAKD FNPKS FVNVHDFNNFDEA I DYIRYLH
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N-PSDB; AEB70134.
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Matches 362;
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                                                                                                                               416 RVNYDDLRVNCDDLRVNYDDLRVNYERLLQNASPLLELSQNTTFKIYRKAYQKSLPLLRA 475
                         406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated alycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a sylycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MFQPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII
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                                             ----DDLRRDHDDLRRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRA
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                         LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY
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                                                                                                                                                                                                                                                                                                  This invention relates to novel isolated polymucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (PutA and PutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
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YLRMPLYYDRLHHKAESVNDTTSPYKLKPDSLYALKKPSHHFKENHPNLCAVVNNESDPL
                                                                                                                                                                                                                          THPNAYLDMLYENPLNTLDGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIF---YRD
                                                                                                                         KRGFASFVASNPNAPIRNAFYDALNAIBPVASGGSVRNTLGYKVKNKNEFLSQYKFNLCF
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                                  LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR
                                                                                                                                    KRGFASFVASNPNAPKRNAFYDALNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCF
                                                                                                                                                                                                                                                                     LNEPLISIDDERVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding fucosyltransferase protein, us for synthesizing oligosaccharide moiety on a protein or lipid that unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                        LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori strain 1182 FutB protein SeqID 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson KF, Bezila DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-123401/12.
N-PSDB; ADJ77809.
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chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to Nactification of actylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to strain 1182 FutB protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                   1 MPOPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKORYKII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                           DB 8; Length 486;
                                                                                                                                                                                                                                                                               48; Indels
                                                                                                                                                                                                                                         77.0%; Score 1892.5; DB 8
75.1%; Pred. No. 1.2e-153;
ive 41; Mismatches 48;
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                                                                                                                                                                                                                                                                                 Matches 361; Conservative
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Best Local Similarity
                                                                                                                                                                                                    Sequence 486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              ENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                               1 MFQPLLDAYIESASIEKITSKSPPPLKIAVANWW--GDEEVEEFKKNILYFILSQHYTIT 58
                                                                                                                                                                     This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                     and
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                                                                                                         Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate acceptor substrate on glycoprotein.
                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                            Length 486;
                                                                                                                                                                                                                                                                                                                 48; Indels
                                                                                                                                                                                                                                                                                          Query Match
77.0%; Score 1892.5; DB 8;
Best Local Similarity 75.1%; Pred. No. 1.2e-153;
Matches 361; Conservative 41; Mismatches 48; 1
                                       (NEOS-) NEOSE TECHNOLOGIES INC
         23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                                                                                                                   Claim 1; Fig 1; 84pp; English
                                                          Johnson KF, Bezila DJ;
                                                                              WPI; 2004-132958/13.
                                                                                        N-PSDB; ADJ27344
                                                                                                                                                                                                                                                                          Sequence 486 AA;
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AEB70131 standard; protein; 486 AA.

RESULT 11 AEB70131 LO AEB7

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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose readiue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
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LNEPLISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD
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                                                                                       Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson KF, Bezila DJ;
                                                                                                                                  protein production; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 2; 97pp; English
                                                                                                                                                                                   Helicobacter pylori; strain 1182
                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                                                                                                                                                             22-JAN-2004; 2004US-00764212
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Best Local Similarity 75.1%
Matches 361; Conservative
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                                           (first
                                                                                                                                       Fucosyltransferase;
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AEB70131;
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RESULT 12 ABG30887

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ABG30882 standard; protein; 485 AA
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                                                                                                                                                                                                                                                                                                                                         Matches 358; Conservative
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                                                                                                                                                                                                                               Sequence 454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002068347-A1.
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                                                                                                                                                                                                                                                                                       Query Match
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ABG30882
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fucosyltransferase polypeptide, having a repeat of the sequence: x_1-x_2-
fucosyltransferase polypeptide, having a repeat of the sequence: x_1-x_2-
cuet-Argx, A=7yr, where x 1, x 2 and X 4 is Asp or Asn; and X 3 is
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                                                     Enzyme; fucT; alphal, 3 fucosyltransferase; oligosaccharide; Lex; Ley; stex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                             LRVNYDDLRVNYDDLRRDHDDLRRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori alphal, 3 fucosyltransferase #7.
                                                                                                                                                                                                                                                                                                                                            ABG30887 standard; protein; 454 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 THPNAYLDMLYENPLNTLDGKAYFYQNLSFKKILDFFKTILENDTIXH---NHPFIFYRD 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDL 416
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|INEPLVSI------DNLRINYDNLRVNYDDLRVNYDDLRVNYDDLRINYDDLRINYDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENSOGYGYVTEKILDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 AHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRD 356
fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple helix sequences and for alphal, 3-fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alphal, 3 fucosyltransferase encood by the fucT gene. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                       58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFQPLLDAFIESADIEKWASKSPPPLKIAVANWW--GDEBIKEFKKSTLYFILSQHYTIT
                                                                                                                                                                                                                                                                                                                                                                                       59 IHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR
                                                                                                                                                                                                                                                                                                                                                                                                             1 MPQPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                  Length 454;
                                                                                                                                                                                                                                                             47; Indels
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                                                                                                                                                                                                                / Match 76.9%; Score 1889; DB 5;
Local Similarity 77.8%; Pred. No. 2.1e-153;
                                                                                                                                                                                                                                                             39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori alphal, 3 fucosyltransferase #2.
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the invention relates a purilled transmemorane segment-rice apprair. C. fucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2 leu-Arg-X_3-X_4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is [11e, Val or Ala. Also included are the nucleic acid encoding the protein (including its complement or fragment), a vector containing the nucleic acid, a host cell containing nucleic acid or vector, an antibody which selectively binds to the protein and a gene expression system for selectively binds to the protein and a gene expression system for comprising a host cell modified with the nucleic acid or its conforting the protein with a substrate such as LackAck. R and GDP-fucose, comparating the protein with a substrate such as LackAck. B by contacting the protein with a substrate such as LackAck. R and GDP-fucose, and purifying the protein with a substrate such as LackAck. R and GDP-fucose, and purifying the protein with a substrate, to produce oligosaccharides, or by culturing the cell, or contacting the protein with a substrate, to produce oligosaccharides and purifying the nucleic acid, by contacting a sample with a nucleic acid using polymerase chain reaction (PCR). The polymucleotide, and detecting hybridisation of the probe; or by polymucleotide, and detecting pyprucleotide encoding a desired polypeptide or polymucleotide, and detecting pyprucleotide encoding a desired polypeptide or polymucleotide, and detecting pyprucleotide encoding a desired polypeptide or polymucleotide under conditions which allow expression and secretion in the crosyltransferase fusion protein, by growing the host cell containing a sample. The protein and isolating the fusion protein. The antibody is useful as manner is an and for inhibiting abnormal alpha1,3-c fucosyltransferase gene product activity. The nucleic acid is useful as useful in the development of assays to detect the protein or cell are useful in the development of assays to detect the protein or cell are useful in the development of assays to detect the p
                                                                                                                                                                                                                                          The invention relates a purified transmembrane segment-free alpha 1,3-
                                                                                                     Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                                                                     Claim 6; Fig 6; 37pp; English
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Taylor DE,
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Sequence 485 AA;

236 AHQNAYLDMLYENPLATIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRD 356 118 176 ENSOGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296 28 239 ENSOGYGYVTEKIIDAYFSHTIPIYWGSPSVAQDFNPKSFVNVCDFKDFDEAIDHVRYLH LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR YLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPW KRGFAS FVASNPNAPI RNA FYDALNA I EPVASGGS VKNTLGYKVKNKNEFLSQYKFNLCP MEQPILIDAFIDSTHIDETTHK--PPINVALANWWPLKNSEKKGFRDFILHFILKQRYKII Gaps 31, DB 5; Length 485; 48; Indels 76.7%; Score 1885.5; DB 5 75.1%; Pred. No. 4.7e-153; tive 41; Mismatches 48; Matches 361; Conservative Local Similarity 29 119 237 297 177 Query Match 셤 ઠે 셤 ઠે 셤 ઠ 셤 ઠે 셤 ò

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Gaps

36;

Length 432; 42; Indels 1 MPQPLLDAPIDSTHLDE-TTHKPPLNVALANWMPLKNSEKKGFRDFILHFILKQRYKIIL 59

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Query Match 73.9%; Score 1817; DB 8; Best Local Similarity 76.7%; Pred. No. 3.1e-147; Matches 352; Conservative 29; Mismatches 42;

Purpopositions thereof, which are related to the fucosyltransferase enzymes (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to Nactylucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to strain 1111 FutA protein sequence of the invention. 299 THPNAYLDMLYENPLNTLDGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIF---YRD 355 454 435 This invention relates to novel isolated polymucleotides and the encoded New isolated polynucleotide encoding fucosyltransferase protein, usefu for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids. 412 ------DHDDLRRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLR Futh, Futh; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; fucose; N-acetylglucosamine; glycoconjugate; enzyme. Helicobacter pylori strain 1111 FutA protein SeqID 4. Claim 16; SEQ ID NO 4; 72pp; English ADJ77812 standard; protein; 432 AA. (NEOS-) NEOSE TECHNOLOGIES INC. 08-NOV-2002; 2002US-0424894P. 23-JUL-2003; 2003WO-US023057 23-JUL-2002; 2002US-0398156P (first entry) Z; Bezila WPI; 2004-123401/12. Helicobacter pylori N-PSDB; ADJ77811 Sequence 432 AA; WO2004009838-A2 476 A 476 455 A 455 Johnson KF, 06-MAY-2004 29-JAN-2004 ADJ77812; RESULT 14 ADJ77812 g g Š ò ò

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                                                                                          LRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPWK 177
                                                                                                                                                                                                NSQGYGYVTEKILDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHA 297
                                                                                                                                                                                                                                                  HONAYLDMLYENPLNTIDGKAGFYQDLSPEKILDFFKNILENDTIYHCNDAHYSALHRDL 357
                                                                                                                                                                                                                                                                                                     NEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLR 417
              58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate
239 NTQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHT
                                                                                                                                                                                                                                                                 HPNAYLDMAYENPLNTIDGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIF---YRDL
                                        HSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRY
                                                                                                                                              RGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVRONTLGYKVKNKONEFLSQYKFNLCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
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|NEPSVSI------DGLRVMYDDLRVMYDDLRVMYDDLRVMY
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                                                                                                                                                                                                                                                                                                                                                                     ---ERLLQNASPLLELSQNTTFKIYRKAYQKSLPLLRAI 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 2; 84pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-2003; 2003WO-US023155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KF, Bezila DJ;
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which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                            1 MPQPLLDAFIDSTHLDE-TTHKPPLNVALANWMPLKNSEKKGFRDFILHFILKQRYKIIL
                                                                                                                                                                                                   1 MFQPLLDAFIESAPLKKWPLNLPPLKIAVANWW--GDEBIKKFKKSVLYFILSQHYTITL
                                                                                                                                                                                                                                                                                                            LRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPWK
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                                                                                                                                                       Gaps
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                                                                                                                           Length 432;
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                                                                                                                         73.9%; Score 1817; DB 8; 76.7%; Pred. No. 3.1e-147; ive 29; Mismatches 42;
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Job time : 122.286 secs
                                                                                                                                        Best Local Similarity 76.74
Matches 352; Conservative
                                                                                             Sequence 432 AA;
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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August 11, 2006, 19:37:09; Search time 21.4069 Seconds (without alignments) 2049.570 Million cell updates/sec Run on:

US-10-764-212-20 2458 1 MFQPLLDAFIDSTHLDETTH......TSFKIYRKAYQKSLPLLRAI 456 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pirl: \* 3: pirl: \* 4: pirl: \* PIR\_80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C82931 T18499 E71604	B97832 A57596 T50364	A71621 H82932 S40259 H96742	H82943 H90567 T18482	AH1879 C71622 S51866
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1084 1619 2380	433 1098	1188 678 910 393	747 912 2437	324 1979 752
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30 31 32	9 9 9 9 5 5 4 9 5	3 3 3 3 4 6 3 6 3 7 8	40 41 42	43 44 5

## ALIGNMENTS

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RESULT 1
B71914
alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A; Variety: strain J99
C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
C,Accession: B71914
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; 7
Nature 397, 176-180, 1999
A, Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <arn></arn>
A;Cross-references: UNIPROT:Q9ZL13; UNIPARC:UP10000003665; GB:AE001491; GB:AE001439; NID:
A,Experimental source: strain J99
C;Genetics:
A,Gene: fucT

'n Gaps Indels 12; Length 454; Query Match 81.6%; Score 2005; DB 2; Best Local Similarity 82.3%; Pred. No. 5.7e-126; Matches 377; Conservative 30; Mismatches 39;

ඊ ඊ		MPQPILIDAFIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILH 60	
Q C	7	MFQPLLDAYTDSTKLDKTDYKFFLNIALANWWFLDAKESKGFKKFILIFILSQKIIIILA 90	
ò	61	SNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYL 120	
qq	61	NFNLFDYAIGFDELDFR	
ò	121	MLVNDTTSPYKLK	
QQ	121	DNSLYALKKPSHHI	
ò	179	GFASFVASNPNAPIRNAFYDALMAIBPVASGGSVKNTIGYKVKNKNEFLSQYKFNLCFEN 238	
qq	181	GFASFVASNPNAPIRNAFYDALNSIBPVTGGGSVRNTLGYN	
δ	239	SQGYGYVTEKILDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAH 298	
q <sub>Q</sub>	241	TQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVCDFKNFDEAIDYVRYLHTH 300	
ò	299	ONAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLM 358	
qq	301	TIYHDNPFIF	
δ	359	EPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRR 418	
đ	358	RVNYDDLRVNYDDLRVNYDDI	

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Ristomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney,
Son, J.D.; Kelley, J.W.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
Allin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A.
A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97394467; PMID:9252185
                                  A,Accession: G71862
A,Status: preliminary
A,Molecule type: DNA
A,Residus: 1-436 <ARN>
A,Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI0000D36D2; GB:AE001528; GB:AE001439; NID:A,Experimental source: strain J99
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Best Local Similarity 72.7%; Pred. No. 6.4e-107;
Matches 335; Conservative 31; Mismatches 45; Indels 50; Gaps
                                                                                                                                                                                                                                                                                       Query Match
73.3%; Score 1801.5; DB 2; Length 436;
Best Local Similarity 75.8%; Pred. No. 1.8e-112;
Matches 350; Conservative 30; Mismatches 41; Indels 41;
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A; Reference number: A71800; MUID: 99120557; PMID: 9923682
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Bacession: G71862
C;Accession: G71862
E;Accession: G71862
E;Acces
                                                                                                                                                                                                                                                                                                                                 C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: G4601
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Redicules: 1-476 <TOM>
A;Cross-references: UNIPROT: O25366; UNIPARC: UPI00000D70CB; GB:AE000578; GB:AE000511; NIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.5%; Score 1929; DB 2; Length 476; Best Local Similarity 77.5%; Pred. No. 6.9e-121; Matches 368; Conservative 39; Mismatches 44; Indels 2.
                                                                                    414 ---RILIQNASPLLELSQNTTFKIYRKAYQKSLPLLRTI 448
                                                                                                                                                                                                                                                                                                      fucosyltransferase - Helicobacter pylori (strain 26695)
                                             419 DHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI
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hypothetical protein C0780w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Doct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18497
R;Lawson, D.; Bowman, S.; Barrell, B.
Submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Reference number: Z18935
A;Accession: T18497
A;Accession: T18497
A;Accession: T18497
A;Accession: T2647
A;Accession: L2657
A;Accession: L2657
A;Accession: L2657
A;Accession: L2657
A;Accession: L2657
A;Accession: L2657
A;Accession: L2657
A;Coss-references: UNIPROT:077380; UNIPARC:UPI000017CC3A; EMBL: Z98551; NID:e1331903; PII
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C;Species: Plasmodium falciparum
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T09079
E;Au. X.z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E.
Cell 91, 593-603, 1997
A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A;Reference number: Z16556; MuID:98054002; PMID:9393853
A;Recession: T09079
A;Recession: T09079
A;Residues: translated from GB/EMBL/DDBJ
A;Residues: 1-2708
A;Residues: 1-2708
A;Residues: UNIRROT:O15791; UNIPARC:UPI000079A61; EMBL:AF030692; NID:g2642513; I
A;Experimental source: strain 7G8; from Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable chloroquine resistance protein CG2 (strain 7G8) - malaria parasite (Plasmodium 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 LLLEYDVK-ENDPITLSKINLCELN---GLHLEE--DVIFLLDBRHKTLLFYGYKNILK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DFNPKSFVNVHDF--NNFDEA--IDYIRYLHAH------QNAYLDMLYENPLNT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 189.5; DB 2; Length 2657; 27.0%; Pred. No. 0.00032; tive 56; Mismatches 110; Indels 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.0%
Matches 90; Conservative
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C;Keywords: toxin resistance
        327 QFKSEGFVQ 335
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A,Map position: 3
A,Note: C0780w
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C; Date: 21.-1an-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C; Date: 21.-1an-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C; Accession: T44227
R; Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
R; Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
R; Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
R; Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
A; Reference number: Z22749; MUID:99453293; PMID:10521656
A; Raccession: T44327
A; Statuus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-346 < YAM>
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179 LKRGFASFVASNANAPMRNAFYDALNSIEPVTGGGSVRNTLGYKVGNKSEFLSQYKFNLC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 FENSQGYGYYTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 HAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR 355
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358 DLHKPLVSI------ 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNDRYLRMPLYYAY-----LHYKAMLV------NDTTSPYKLKALYTL-----K 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 PSVAKDFNPK-SFVNVHDFNNFDEAI------DYIRYLHAHQNAYLDMLYENPLNTI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 HTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHKFSTSF-MMEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 DLNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RLLQNASPLLELSQNTTFKIYRKAYQKSLPLLRAV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 LRRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein wbfL [imported] - Vibrio cholerae
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probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium f
C;Species: Plasmodium falciparum
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-2819 <SUX>
A;Cross-references: UNIPROT:O15792; UNIPARC:UPI0000785E5; EMBL:AF030693; NID:g2642515; I
A;Experimental source: strain HB3; from Honduras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chin, C.W.; Chung, M.K.; Conn, L.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
                                                                                                                            R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E.
Cell 91, 593-603, 1997
A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A;Reference number: Z16556; MUID:98054002; PMID:9393853
A;Accession: T09080
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 QNTKRVPYTGENEVPNFNLFDYAIGF-----DELDFNDRYLRMPLYYAYLHYKAMLV- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable fucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      920 D---NWADQGGNANDHDDNANNHDDDNANNHDDSWANHDDNWANHDDNWANHDDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 NLCFENSQ--GYGYVTEKILDAYFSH----TIPIYWGSPSVAKDFNPKSFVNVHDFNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     752 KKENENSYILRYTFYNQKI-DLPINMINEKLVPKCHWDS------DIFINMISLSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DFPKNI-----LEN----DTIYHCNDAHYSALHRDLNEPLVS---VDDLRRDHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 BLK-----CODTNGNIK---FDQMN-----DHVKNDHTNYYQNNNIFNLLTLIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 DLRVNYDDLRVN---YDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRRDHERLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 KNSEKKGFRDFILHFILKO------RYKIILHSNPNEPSDLVFGNPLEQARKILSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 155; DB 2; Length 2819;
Best Local Similarity 21.7%; Pred. No. 0.069;
Matches 113; Conservative 69; Mismatches 173; Indels 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: cg2
C;Keywords: toxin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: F96533
                                                                                                                C;Accession: T09080
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A;Cross-references: UNIPROT:Q92GR3; UNIPARC:UPI0000CBFA7; GB:AE006914; PIDN:AAL03597.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, 098, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: C97832
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Pournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 GYKV--KNKNEFLSQYKFNLCPENSQGYGYVTEKILDAYPSHTIP-IYWGSPSVAKDFNP 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          746 KKENENSYILRYTFYNQKI-DLFINMINBKLVFKCHWDS-----DIFINMISLSYN 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEAIDYIRYLHAHQNAYLDMLYENPL-------330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DFFKNI-----LEN-----DTIYHCNDAHYSALHRDLMEPLVS---VDDLRRDHD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           914 DIMINDQGGNMINHYDIMINI-HIDDIMININHDDIMINHHDDIMINKHTHYL 972
                                                                                                                85 QNTKRVFYTGENEVPNFNLFDYAIGF-----DELDFNDRYLRMPLYYAYLHYKAMLV- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-----LRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRRDHERLL 424
                                                      55 KNKNK----IILKFILNNLNGNIQVFMLPFSYPSNKKKKKKKKNIFKN-----ILSY 602
                                                                                                                                                                                                                                137 ------NDTTSPYKLKALY----TLKKPSHKPKENHPNLCAL-----IHNESD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-(1,3)-fucosyltransferase homolog RC1059 [imported] - Rickettsia conorii
C,Species: Rickettsia conorii
C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVLAYKRSKYNPNKTYFACFLVSNGIEEPENDGCIARNRFFHKLSLYKKVVSGSKYLNTE 62
                                                                                                                                                    644 FSILKIFCTCDDDTTLLISRKHVYYLSDSLEKSEYSYKTGVINIHDLLLDYFFDLHFIKD
                                                                                                                                                                                                                                                                                                                                                      175 PWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEF--LSQYKF
                                                                                                                                                                                                                                                                                                                                                                                       704 ELK-----CQDTNGNIK---YDQMN-------DHVKNDHTNYYQNNNIFNLLTLIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 NLCFENSQ--GYGYVTEKILDAYFSH-----TIPIYWGSPSVAKDFNPKSFVNVHDFNNF
KNSEKKGFRDFILHFILKQ------RYKIILHSNPNEPSDLVFGNPLEQARKILSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973 NDKDNYNSKGTFPENTLDDKKNCSYQKNFVSVFYFTIYVNKNTPLL 1018
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ribosome releasing factor (OO, TP) PFB0390w [imported] - malaria parasite (Plasmodium fall NiAlernate names: ribosome recycling factor Cippecies: Plasmodium falciparum falciparum falciparum falciparum falciparum (Cipate: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 Rigardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Spertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Oulmouden, A.; Wierinckx, A.; Petit, J.M.; Julien, R. submitted to the EMBL Data Library, June 1995
A.Description: Molecular cloning and expression of bovine alpha (1,3/4)-fucosyltransferate A.Reference number: $55498
A.Reference number: $55498
A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-365 <0UL>
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A;Cross-references: UNIPROT:096173; UNIPARC:UPI00000786F0; GB:AE001391; GB:AE001362; NID: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum
A;Reference number: A71600; MUID:99021743; PMID:9804551
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   241 GYGYVTEKILDAYPSH--TIPIYMGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAH 298
                                                                                                                                                                                                                                                                                       344 HCNDAHYSAL----HRDLNEPL-----VSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYD 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                alpha(1,3/4)-fucosyltransferase - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
                                                                         622 IHNNNSSYLQNNNIFHLSDILLY-----YMKKDYIKIYBFLTFRTIIEKRQMTNLM
                                                                                                                                               299 QNAYLD------MLYENPLNTIDGKAGFYQDLSFEKILDFFK---NILENDTIY
                                                                                                                                                                                        196 FYDALNAIBPVASGGSVKNTLGYKV--KNKNEFLSQYKF-NLCFENSQGYGYVTEKILDA
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|-----INITKRETV----
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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosomel of the plant Arabidopsis.
A;Reference number: A86141; MUD:21016719; PMID:11130712
A;Accession: P6553
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A;Gene: F14J22.8
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1532 <LAW>
A;Cross-references: UNIPROT:077332; UNIPARC:UPI000017CC26; EMBL:Z98547; NID:e1325376;
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 LWNSFISNLFKDEYIYM-----LMNEIKKANNKKHIVHEEEFITYLKQIKLLQL 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DFNDRYLR 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : |: || : |: || 526 IYTWRQYIFYKTYMNKQREKEKSIKSNNYYMNIFDDMNNEN-----LINFETDP----- 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 DYIRYLHAHQNAYLDML---YENPLNTIDGKAGFYQDLSFEKILD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 KRMKYLAANPAAYNQTLRWKYEGPSD-----SFKALVD 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 147.5; DB 2; Length 930.9%; Pred. No. 0.023; Live 30; Mismatches 57; Indels
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A;Note: C0415c
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Best Local S
Matches 51
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A;Reference number: 220560
A;Recession: T29091
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1840 <COL-
A;Cross-references: UNIPROT:Q90831; UNIPARC:UPI00000FC683; EMBL:X80877; NID:g1279430; PI
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C;Species: Gallus gallus (chicken)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34073
R;Hemken, P.M.; Bellin, R.M.; Sernett, S.W.; Becker, B.; Huiatt, T.W.; Robson, R.M.
A;Hemken, P.M.; Bellin, R.M.; Sernett, S.W.; Becker, B.; Huiatt, T.W.; Robson, R.M.
A;Reference number: Z214399, 1997
A;Reference number: Z21471; MUID:98070426; PMID:9405460
A;Accession: T34073
A;Accession: T34073
A;Accession: T34073
A;Accession: T6063
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A;Cross-references: UNIPROT:Q9TQQ3; UNIPARC:UP10000088B27; EMBL:X87810; NID:g860807; PID
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29091
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090ku3 plasmodium
05f210 drosophila
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                                                                                              August 11, 2006, 19:30:58 ; Search time 160.382 Seconds
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1 MFQPLLDAFIDSTHLDETTH.....TSFKIYRKAYQKSLPLLRAI
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O54ph9 0
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                   2849598 seqs, 925015592 residues
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030511 HELPY
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O34231_VIBCH
Q9NFU3_PLAFA
Q5F2L0_DROYA
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Q8I297_PLAF7
Q8IKL3_PLAF7
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1: uniprot sprot:*
2: uniprot_trembl:*
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Q815d1 Q54pk3 Q6a2m3	Q6q5y3 Q98t51 Q599j4 O15791	Q8ikl6 Q7p9h9 Q54bb7 Q8ijh4	Q6ale3 Q8iec4 Q333x7
Q8L5D1_PHYPA Q54PK3_DICD1 Q6A2M3_PHYPA	Q6Q5Y3_MEDTR Q9ST51_PHAAU Q599J4_9ROSI O15791_PLAFA	Q8IKL6_PLAF7 Q7P9H9_RICSI Q54BB7_DICDI Q8IJH4_PLAF7	Q6A1E3_CIOSA Q8IEC4_PLAF7 Q333R7_DROER
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168.5 167.5 166.5	166 165.5 165.5	164.5 164 163 162	161.5 161.5 160.5
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## ALIGNMENTS

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GO; GO:0016020; C:membrane; IRA.

GO; GO:0008417; F:fucosyltransferase activity; IRA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:001686; P:protein amino acid glycosylation; IRA.

InterPro; IPR001503; Glyco_trans_10.

PANTHER; PTHR11929; Glyco_trans_10; 1.

Glycosyltransferase; Transferase.

SEQUENCE 462 AA; 54560 MW; BD27F8B351ECE752 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-UA948;
MEDINE-2013842; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
"Cloning and characterization of the alpha(1,3/4) fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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                                                        01-077-2000, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 2. 07-FEB-2006, entry version 17. Alpha-1,3/4-fucosyltransferase.
462 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Helicobacter pylori.";
J. Biol. Chem. 275:4988-4994(2000).
PRT;
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PRELIMINARY;
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Matches 456; Conservative
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181 GFASFVASNPNAPIRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEPLSQYKFNLCFEN 240
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016486; P:protein anino acid glycosylation; IEA.
InterPro; IPR01503; Glyco_trans 10.
InterPro; IPR01503; Glyco_trans 10.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 476 AA; 55927 MW; 312BFPDBBD36EIF74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=26695 / ATCC 700392;
MEDLINE=9739467; PubMed=9252185; DOI=10.1038/41483;
Tomb J.-F., White O. Kerlawage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Bougherty B.A., Nelson K.B., Quackehbush J., Zhou L., Kirkness B.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kallin B., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
                                                   RMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPWKR
                                                                              SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAH
                                                                                                                                                           GFASFVASINPNAPIRNAFYDALNAI EPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=HP0651; ORFNames=HP_0651;
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the gastric pathogen Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fucosyltransferase.
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     121 RMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGF 180
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                                                      181 ASFVASNPNAPIRNAFYDALMAIEPVASGGSVKWTLGYKVKNKNEFLSQYKFNLCFENSQ
                                                                                 181 ASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTILGYKVKNKNFFLSQYKFNLCFENSQ
                                                                                                                                                             GYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQN
                                                                                                                                                                                                                                                                     AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA (1,3)-PUCOSYLTRANSFERASE.
Mame-fuct; ORNames-jhp 0596;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacterae; Helicobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraes; Helicobacteraes;
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"Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006486; F:protein amino acid glycosylation; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0016486; F:protein amino acid glycosylation; IEA.
Interpro; IPRO1503; Glyco trans 10.
PANTHER, PIRR11929; Glyco trans 10; 1.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64;
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Matches 377; Conservative 30; Mismatches 39; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI 456
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Query Match

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Q9zli3\_HELPJ Q9zli3;

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Query Match

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Gaps

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RYLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDP 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NCTC 11639; MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357; MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357; Ge Z., Chan N.W.C., Pablcic M.M., Taylor D.B.; "Cloning and hererologous expression of an alpha1,3-fucosyltransferase gene from the gastric pathogen Helicobacter pylori."; J. Biol. Chem. 272:21357-21363(1997).
                                                                                                                                                             TLHONPNESSDLVFSNPLGAARKILSYQNTKRVFYTGENESPNFNLFDYAIGFDELDFND
                                                                                                                                                                                                                                                                                         299 HTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFIF---YR
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|DLHEPLISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD
                                                                                                                                  58 ILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFND
                                                                                                                                                                                                                                                                     WKRGFASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNEFLSQYKFNLC
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                                                                  1 MFOPLLDAFIDSTHLDETTHK---PPLNVALANWWPLKNSEKKGFRDFILHFILKORYKI
                                                                                  FENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYL
                                                                                                                                                                                                                                                                                                                                                                                                          HAHONAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016417; F:transferase activity; IEA.
GO; GO:0016757; F:transferase activity; transferring glycosyl.
GO; GO:0006466; P:protein amino acid glycosylation; IEA.
InterPro; IPR01503; Glyco_trans 10.
PANTHER, FTHR11929; Glyco_trans 10.
Glycosyltransferase; Transferase.
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78.5%; Score 1929; DB 2; Length 476; 77.5%; Pred. No. 1.1e-118;
                               44; Indels
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ID O30511 HELPY

AC 030511,
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-DFB-2006, entry version 26.
DE Alpha1,3-fucosyltransferase.
             Pred. No. 1.16 39; Mismatches
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                                 368; Conservative
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               Similarity
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                                                                                                                                                                  ENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
                                                                                                                                                                                                                                                                             297 AHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRD 356
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Distributed under the Creative Commons Attribution-NoDerivs License
                                      1 MFQPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII
                                                     KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016475; F:turansferase activity, transferring glycosyl.
GO; GO:0016486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
PANTHER; PTHR11929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 432 AA; 50503 MM; 69D3A32FBD2F12C9 CRC64;
           23;
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            Indels
              45;
Pred. No. 6.5e-118;
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Pred. No. 1.3e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbani S., Miksa V., Wipf B., Ernst B., "Molecular Cloning and Functional Expression pylori (alpha)-1,4 Fucosyltransferase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=16000696; DOI=10.1093/glycob/cwj004;
           41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
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07-FEB-2006, entry version 8.
Alpha-1,4 fucosyltransferase.
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77.0%;
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           Matches 365; Conservative
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STRAIN=DSM 6709;
Best Local Similarity
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Best Local Similarity
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Q6ST35;
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O25142;
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357 EPLVSI-------DDLRINYDDLRINYDDLRINYDDLRINY------390
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G0; G0:0016020; C:membrane; IEA.

G0; G0:0016757; F:fucosyltransferase activity; IEA.

G0; G0:0016757; F:fucosyltransferase activity, transferring glycosyl. . .; IEA.

G0; G0:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

G0; G0:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

G0; G0:0016757; F:transferase activity, transferase.

G1ycosyltransferase.

Complete proteome; G1ycosyltransferase.

ECMPLER: A16 AA; 50699 MM; IDB2066AE98FAGIE CRC64;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                   GFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKNEFLSQYKFNLCFEN
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MEDLINE=99120557; PubMed=9921682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Viria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                      1 MFQPLLDAYIDSTRLDETDYKPPLKIAVANWW----GGVEEFKKSTLYFILSQRYTITLH
                                                                                                                                            61 SNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYL
                                                                                                                                                                        RMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPWKR
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                                             1 MFQPLLDAFIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRR
Gaps
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Nature 397:176-180(1999).
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02-XD7;
01-MAY-1999, integrated into UniProtKB/TrEMBL.
01-MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA-(1,3)-PUCOSYLTRANSPERASE.
Name=fucU; ORFNames=jhp 1002;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
34;
33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 --ERLLONASPILELSONTSFKIYRKAYOKSLPLLRAI
32; Mismatches
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  Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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STRAIN=26695 / ATCC 700392;
STRAIN=27394467; PubMed=9252185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.N., Nelson K.B., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Watthey J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
                                                                                                                                                    1 MFQPLLDAFIESTPIKKKITFKSPPPPLKIAVANWW----GGAEBFKKSTLYFILSQRYT
                                                                                                                                                                                                                                 57 IILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFN
                                                                                                                                                                                                                                                               CPENSOGYGYVTEKILDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 CFENTQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVCDFKNFDEAIDYVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 LHAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 RDINEPLVAI-------DDLRVNYDDLRVNYDDLRVNYDDLRVNYD-----
                                                                                                                1 MFQPLLDAFIDSTHL-DETTHK---PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYK
                                                                                                                                                                                                                                                                                                                                                  DRYLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESD
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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     DB 2; Length 436;
                                                           Indels
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73.3%; Score 1801.5; DB 2, 75.8%; Pred. No. 2.5e-110; ive 30; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998, integrated into UniProtKB/TrEMBL. 01-JAN-1998, sequence version 1. 07-PEB-2006, entry version 24. Pucosyltransferase.
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                                Best Local Similarity 75.88 Matches 350; Conservative
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                                                                                                                                                                                                                                                                                                                   RYLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDP 175
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                                                                                                                                                                                                                        58 ILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFND
                                                                                                                                                              1 MFQPLLDAFIDSTHLDETTHK---PPLNVALANWWPLKNSEKKGPROFILHFILKQRYKI
                                                                                                                                                                           1 MFQPLLDAFIESASIEKWASKSPPPLKIAVANWW--GDEEIKEFKKSVLYFILSQRYAI
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Bird M.I.;
"Lewis X biosynthesis in Helicobacter pylori. Molecular cloning
       GO, GO:0016020; C:membrane; IEA.
GO; GO:0008417; P:fucosyltransferase activity; IEA.
GO; GO:001677; P:transferase activity; IEA.
GO; GO:0016486; P:protein anino acid glycosylation; IEA.
InterPro; IPR001503; Glyco trans 10.
PANTHER, PTRR11929; Glyco trans 10.
COMplete proteome; Glycosyltransferase; Transferase.
SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;
                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=NCTC 11637;
MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
                                                                                                                 Length 425;
                                                                                                      69.9%; Score 1718; DB 2; Leugum .-72.7%; Pred. No. 7.7e-105; Lindels
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01-JAN-1998, integrated into UniProtKB/TrEMBL
01-JAN-1998, sequence version 1.
07-FBB-2006, entry version 23.
Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-).
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J. Biol. Chem. 272:21349-21356(1997).
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                                                                                                               Query Match
Best Local Similarity 72.74
Matches 335; Conservative
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122 MPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDPWKRG 179
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|-----DNLRINYDNLRVNYDDLRVNYDDLRVNYDDLRINYDDLRINYDDLRINYDDLRIN 290
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FASFVASNANAPFRNAFYDALNSIEPVTGGAVKOTLGYKVGNKSEFLSQYKFNLCFENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 FASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNFFLSQYKFNLCFENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
EMBL; AF006039; AAB93985.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:001686; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
PANTHER; PTHR1929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 333 AA; 39154 MW; CFFCBIAC127E0A8C CRC64;
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Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                  Length 333;
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016746; P:protein amino acid glycosylation; IEA.
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07-FEB-2006, entry version 6.
Putative LPS biosynthesis related glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 YERLLQNASPLIELSQNTSFKIYRKIYQKSLPLLRVI 327
                                                                                                                                                                                                                                                                                                                                           Ouery Match 59.1%; Score 1452; DB 2; Best Local Similarity 81.6%; Pred. No. 1.9e-87; Matches 275; Conservative 26; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 HERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2005, integrated into UniProtKB/TrEMBL
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GO; GO:0006486; P:protein amino
InterPro; IPR002105; Dockerin 1
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Q5L9SG_BACFN PRELIMINARY;
Q5L9SG;
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PRELIMINARY;
                         34.1%;
                                      Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=290397;
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Q2IE19;
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                                                                                                                                                                                                                                                    210
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                                                                                                                                                                                            98 VPNFNLPDYALGFDELDFNDRYLRMPLYYAY----LHYKAMLVNDTTSPYKLKALYTLK 152
                                                                                                                                                                                                                                                                   ------DRKPCSIVVSNNKWADPIRETFFKLLSSYKKVDSGG 161
                                                                                                                                                                                                                                                                                                                                                               FNPKSFVNVHDFNNFDEAIDYIRYLHAHQNAYLDMLYENP----LNTIDGKAGFYQDLSF 326
                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                        26 GP-DTISNFIVDALSIQYEVVLSNEPDYLFYSCRGT-----SHLEYDCIK-IMFIGENI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                       41 GFRDFILHFI---LKQRYKIILHSNPNEPSDLVFGNPLEOARKILSYQNTKRVFYTGENE
                                                                                                                                                                                                                                                    153 KPSHKFKENHPNLCALIHNESDPWKRGFASFVASNPN--APIRNAFYDALNAIEPVASGG
                                                                                                                                                                                                                                                                                                           211 SVKNTLGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKD
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 51449 / 3B1;
MBDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
MBDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
Sucrbaum S., Josenhans C., Sterzenhach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Rischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mandz G.,
Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                           71;
                                                                               Query Match 18.7%; Score 460.5; DB 2; Length 331; Best Local Similarity 36.8%; Pred. No. 3.6e-22; Matches 120; Conservative 44; Mismatches 91; Indels 71.
InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10; 1.
PROSITE; PS000448; CLOS_CELLULOSOME_RPT; UNKNOWN_1.
Complete proteome; Transferase.
SEQUENCE 331 AA; 39181 MW; 679FA409DF8CB864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter hepaticus.";
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003, integrated into UniProtKB/TrEMBL, 01-OCT-2003, sequence version 1. 07-FEB-2006, entry version 12. Alpha-1,3-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=HH1776; ORFNames=HH_1776;
                                                                                                                                                                                                                                                                                                                                                                                                                                     272 OLLLINFINNIMMKSYKDAKYLVNYGH 297
                                                                                                                                                                                                                                                                                                                                                                                                                      EKILDFFKNIL---ENDTIYHCNDAH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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NCBI_TaxID=32025;
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Q7VFA1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
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                                                                                                                       78
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 THKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILHSNPNEPSDLVFGNPLEQA
                                                                                                                                                          8 THKPTKKVYFC----DGAVKG----KIVALLEQHYELIL---TNKDPDYIFYSCM--G
                                                                                                                                                                                                                                           79 RKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYLRMPLYYAYLHYKAMLVND
                                                                                                                                                                                                                                                                           53 FEHLNY-NXVRIFATGENLRADFNFCDYAIGYDYIHFEDRYLRYPL---YLHCESDMQK-
                                                                                                                                                                                                                                                                                                                                                                                                      258 IPIYWGSPSVA-----KDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQNAYLDMLYENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US DOE Joint Genome Institute;

Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israel S., Pitluck S., Brettin T., Bruce D., Han C.,
Tapia R., Gilna P., Kiss H., Schmutz J., Larimer F., Land M.,
Kyrpides N., Anderson I., Sanford R.A., Ritalahti K.M., Thomas H.S.,
Kirby J.R., Zhulin I.B., Loeffler F.B., Richardson P.;
"Complete sequence of Anacromyxobacter dehalogenans 2CP-C.";
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 DALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 DPLSQYNRVDSGGRYKNNIGNPVVDKYAFLKEGKFNIAFENSSTNGYITEKLIQAFAAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 LNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 V------FLDKNHQKIFD---EKLENFLLHIFNQPLEKAYRRGFGQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.1%; Score 345.5; DB 2; Length 287; 28.4%; Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2006, sequence version 1.
07-MAR-2006, entry version 1.
07-MAR-2006, entry version 1.
ORFNames=Adeh_3056;
Anseromyxobacter dehalogenans 2CP-C.
Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Mismatches 113; Indels
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                                                        49; Mismatches 117;
   17.8%; Score 437; DB 2; 34.1%; Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2006, integrated into UniProtKB/TrEMBL
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                                  Pred. No.
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PubMed=15875012; DOI=10.1038/nature03481;

Raichinger L., Pachebat J.A., Glocekner G., Rajandream M.A.,

Bichinger L., Pachebat J.A., Glocekner G., Szafranski K., Xu Q.,

Rucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

Rankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,

Rethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

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Rethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Rethornou A., Nie X., Hall N., Majard C., Hemphill L., Bason N.,

Rooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

Muzny D.M., Mourier T., Pain A., Iu M., Harper D., Lindsay R.,

Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,

Ruights A., Loulseged H., Mungall K.L., Oliver K., Price C.,

Knights A., Loulseged H., Mungall K.L., Oliver K., Price C.,

A ringhts A., Usubhinara H., Hernandez J., Rabbinowitsch B., Steffen D.,

Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,

Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,

Cox B.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,

Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
                                                                                                                                                     132 KAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNBSDPWKRGFASFVASNPNAP 191
                    PRFLL------ERREDVNAIVAE----KTRFCNLVCSNRAAR 131
                                                                 192 IRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKILD 251
                                                                                   132 ERLRFPEKUSRYKPVDSGGRVRNNVGGPVXDKTAFIRQHRFTIAFENASYPGYTTEKIVE 191
                                                                                                                                  252 AYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQNAYLDMLYENPL 311
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004417; F:fucosyltransferase activity; IEA.
GO; GO:000446; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco trans 10.
PANTHER; PTHR11929; Glyco trans 10.
Glycosyltransferase; Golgī stack; Hypothetical protein; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                  312 NTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNEP 360
                                                                                                                                                                                                                                     -----FSTPREDARPP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome of the social amoeba Dictyostelium discoideum."; Nature 435:43-57(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 AA; 54815 MW; 444843FFBAEF6D77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                   Q54PJ9 DICDI PRELIMINARY; PRT; 462 AA. Q54PJ9; 24-MAY-2005, integrated into UniprotKB/TrEMBL 24-MAY-2006, entry version 1. Hypothetical protein. Hypothetical protein.
                                                                                                                                                                                                                   252 P--EGRPTPYSDPGV--LLDWLERV---
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DB 2; Length 462;

8.9%; Score 218;

Query Match

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                                                                                                                                                                                                                           96 NEVPN-----FNLFDYAIGFDELDFNDRYLRM----PLYYAYLHYKAMLVNDTT-- 140
                                                                                                                                                                                                                                                                                                                                                          141 -SPYKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGFASFVASNPNAPIRNAFYDA 199
                                                                                                                                                                                                                                                                                                                                                                                              232 QTQFKLE.-YQVMKHNNTLQP------HQKSIPLANWFCTNCNSHSN---RNEYVQE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 LDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHONAYLDM-LYE 308
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                             40 KGFRDFILHFILKQRYKIILHSNPNEPSDLVFGN----PLEQARKILSYQNTKRVFYTGE
                                                                                                                                                         124 KGLDDKFYYIVRKPYY-----PNOKLDMEIWSDYIVDFEAPKKKKLSSRNVPRTLISME
                                                                                                                                                                                                                                                                   177 PQ-PNRTCEFDKDCFEFFNFKVSFB----SQSDIRMGFDTPSSSAYKLYNKLTIDEIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 LNAIEPVAS-GGSVKNT-----LGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 LMKFIVVDSFGKCLKNMPTSNFLSRGSGDPFBRRKLPITRYKFTIVPENSICKDYVSEKV
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La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
Drancourt M., Birtles R., Claverie J.M., Raoult D.;
                                 78;
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PubMed=15486256; DOI=10.1126/science.1101485;
Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata La Scola B., Susan M., Claverie J.-M.;
"The 1.2-megabase genome sequence of Mimivirus.";
Science 306:1344-1350(2004).
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Best Local Similarity 24.9%; Pred. No. 5e-06;
Matches 85; Conservative 53; Mismatches 126; Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0006486; P:fucosyltransferase activity; IEA.
InterPro; IPR001503; Glyco_trans 10.
PANTHER; PTHR11929; Glyco_trans_10; 1.
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600 AA; 70731 MW; 123F17F7591E9DD9 CRC64;
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07-DEC-2004, sequence version 1.
FEB-2006, entry version 8.
Hypothetical protein.
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QSUQ63;
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ORFNames=MIMI_R654;
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InterPro; IPR001503; Glyco trans 10.
PANTHER; PTHR11929; Glyco trans 10; 1.
Glycosyltransferase; Golgī stack; Hypothetical protein; Transferase;
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A Sichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,

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Rarbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,

A Rarbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,

A Musser H., James K.D., Quiles M., Madan Babu M., Saito T.,

Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,

Ruights A., Loulsaged H., Hernandez J., Rabbinowitsch E., Steffen D.,

Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,

Tivey A., Sugano S., White B., Walker D., Woodward J.R., Wlinckler T.,

Tivey A., Sugano S., White B., Walker D., Woodward J.R., Wlinckler T.,

Cox E.C., Chisholm R.L., Gibbs R.A., Weinstock G.M., Rosenthal A.,

Kaya, R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
                                                                                                                                                                 421 ------KPKTKF------CAYMYNMRYPHRIWYPNLVSK-------YRQVDALG 455
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                                                                                                                                                                                                                                                                                     259 PIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQNAYLDM----LYENPLNTI 314
                           GENEVPNFNLFDYAIGFDELDFNDRYL---RMPLYYAYL-----HYKAMLVNDTTSPYK 144
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                                                                                          145 LKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIE
                                                                                                                                                                                                                205 PVASGGSVKNTLGYKVKNKN-----BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTI
                                                                                                                                                                                                                                      NSEKKGFRDFILHFILK--QRYKIILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYT
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-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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GO:0016020; C:membrane; IEA. GO:0008417; F:fucosyltransferase activity; IEA. GO:0006486; P:protein amino acid glycosylation; IEA.

EMBL; AAF101000108; EAL65160.1; -; Genomic\_DNA. GO; GO:0016020; C:membrans; IEA. GO; GO:0008417; F:fucosyltransferase activity; GO; GO:0006486; P:protein amino acid glycosylat

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e genes responsible for O-antigen synthesis of Vibrio cholerae 0139 closely related to those of Vibrio cholerae 022.";
                                                                                                                                         123 GGLYRFEGDSNFIISNFNI---TVGYPRVNDFNKQTHIYVP--YGPVEYSG-----SDS
                                                                                                                                                                                                                                                                           143 YKLKALYTLKK--PSHKFKENHPNLCALIHNESDPWKRGFASFVASNPNAPIRNAFYDAL
                                                                                                                                                                                                                                                                                                112 YAHSAKFDRIKBIPS----RANN----SIVWISSNCWHBDYK------RVYLMRSI
                                                                                                                                                                                                                                                                                                                                                         201 NAIBPVASGGSVKNTLGY-----KVKNKNBFLSQYKFNLCFENSQGYGYVTEKILD
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MEDLINE=99453293; PubMed=10521656; DOI=10.1016/S0378-1119(99)00344-3;
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Vibrionaceae; Vibrio.
                                  Query Match 8.0%; Score 196.5; DB 2; Length Best Local Similarity 23.9%; Pred. No. 0.00011; Matches 80; Conservative 57; Mismatches 111; Indels
                                                                                                                 52 KORYKIILHSN-PNEPSD-----LVFGNPLEQARKILSYQNTKRVF
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

GO; GO:0006486; P:protein amino acid glycosylation; IEA.

InterPro; IRR001503; Glyco_trans_10.

PANTHER; P
389 AA; 45383 MW; 9EA7D88C3D423F99 CRC64;
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087156;
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153 KDSHKFKENHPNLCALIHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSV 212
                                                                                            64 NMPKILPLPEHIKKSYLILSESAFIRPDNYDANKHAYFN-----KVFTWS---DDLV 112
                              115 FNDRYLRMPLYYAY-----LHYKAMLV------NDTTSPYKLKALYTL-----K 152
                                                                       64 NEPSDLVFGNPLEQARKILS-----YQNTKRVFYTGENEVPNFFDYALGFDELD 114
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299 THKNAYLDMLYENPLNTLDGKAYFYQNLSFKKILAFFKTILENDTIYHDNPFIFC---RD 355
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/ FMC_Celerra_SIDS3/ptcdata/2/jaa/6_COMB.pep:*
/ FMC_Celerra_SIDS3/ptcdata/2/jaa/7_COMB.pep:*
/ FMC_Celerra_SIDS3/ptcdata/2/jaa/H_COMB.pep:*
/ FMC_Celerra_SIDS3/ptcdata/2/jaa/PCTUS_COMB.pep:*
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Listing first 45 summaries

    protein search, using sw model

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79.3%; Pred. No. 4.9e-180;
tive 41; Mismatches 45;
Sequence 1. Application US/09092315
| Patent No. 639937
| GENERAL INFORMATION:
| APPLICANT: Taylor, Diane E.
| APPLICANT: Taylor, Diane E.
| APPLICANT: Ge, Zhongming | TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE | TITLE OF INVENTION: 1094/049001
| CURRENT APPLICATION NUMBER: US/09/092,315 | CURRENT FILING DATE: 1998-06-05 | EARLIER APPLICATION NUMBER: US 60/048,857 | EARLIER APPLICATION NUMBER: US 60/048,857 | SARLIER FILING DATE: 1997-06-06 | NUMBER OF SEQ ID NOS: 22 | SOFTWARE: PastSEQ for Windows Version 3.0 | SEQ ID NO! 1464
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Helicobacter pylori
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Matches 365; Conservative
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
CURRENT APPLICATION WUMBER: US/09/733,524A
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PLILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASKEN OF WINDOWS Version 4.0
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LNEPLVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDL 416
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                                                                                                                                                                                  Sequence 1, Application US/09733524A Patent No. 6534298 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Helicobacter pylori
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, C. Longming
TITLE OF INVENTION: PUCCSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REPERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FEALSEQ for Windows Version 4.0
SEQ ID NO: 27
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78.7%; Score 1934.5; DB 2; Length 464;
Best Local Similarity 79.3%; Pred. No. 4.9e-180;
Matches 365; Conservative 41; Mismatches 45; Indels 9;
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Patent No. 7029891
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
APPLICANT: UNIVERSITY OF APPLICANT:
FILE OF INVENTION: Alpha-1,3 Pucosyltransferase
FILE SPERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/392,098A
1, Application US/10189977A
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US-10-392-098A-1
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US-09-733-524A-5
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US-09-092-315-5
LENGTH: 476
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Best Local Similarity 79.3%; Pred. No. 4.9e-180;
Matches 365; Conservative 41; Mismatches 45; Indels 9;
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: H. pylori strain NCTC11639
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-1
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GENERAL INCORNATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge. Zhongmaing
TITLE OF INVENTION: ALFHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
EARLIER FILING DATE: 1997-06-06;
RARLIER FILING DATE: 1997-06-06;
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
        PRIOR PLINA DATE: USJUGITATION NUMBER: USJUGITATION NUMBER: US 0.040, PRIOR PILING DATE: 2002-04-09

PRIOR PILING DATE: 1002-04-09

PRIOR PILING DATE: 1997-06-06

PRIOR PILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR PILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 1

LENGTH: 464
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2003-03-17
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Helicobacter pylori
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GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US 09/092,315

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 5

SEQ ID NO 5
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                                                                                        Length 476;
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;; Pred. No. 1.8e-179;
39; Mismatches 44;
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                                                                                           Query Match 78.5%;
Best Local Similarity 77.5%;
Matches 368; Conservative 3
TYPE: PRT
ORGANISM: Helicobacter pylori
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Matches 368; Conservative
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TYPE: PRT
ORGANISM: Helicobacter pylori
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Matches 368; Conservative
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Faceure 10. 6962806

GENERAL INFORMATION:

APPLICANT: Taylor, Diane B.

APPLICANT: Taylor, Diane B.

APPLICANT: Taylor, Diane B.

TITLE OF INVENTION: PUCCESTRASER AND EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT APPLICATION NUMBER: US/09/733,524

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR PLIING DATE: 1998-06-05

PRIOR PLIING DATE: 1998-06-05

PRIOR PLIING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PASSEQ for Windows Version 4.0
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                                58 ILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYALGFDELDFND
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1 MFQPLLDAFIESASIEKON/SKSPPPPLKIAVANWW--GDEEIKEFKKSVLYFILSQRYAI
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ORGANISM: Helicobacter pylori
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176 WKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLC
                     FENSOGYGYVTEKILDAYFSHTIPIYMGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYL
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OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: University of Alberta
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpa-1,3 Fucosyltransferase
FILE REFERENCE: 017399-000420US
CURRENT APPLICATION NUMBER: US/10/120,319
PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR FILING DATE: 2002-04-09
PRIOR PLING DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Ratentin Ver. 2.1
SEQ ID NO 5.
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; Patent No. 7029891
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GENERAL INFORMATION:
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                                                            HAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR 355
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1999-06-05
BEALIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09092315
Patent No. 6399337
GENERAL INFORMATION:
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US-09-092-315-7
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION NUMBER: US/09/733,524A
CURRENT FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASISEQ for Windows Version 4.0
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Patent No. 6962806
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: PUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
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Sequence 7, Application US/09733524A
Patent No. 6534298
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US-09-733-524A-7
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PRIOR APPLICATION NUMBER: US 09/733,524
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Best Local Similarity
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TYPE: PRT
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Refert No. 702991
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1.3 Pucosyltransferace;
TILE REFERENCE: 017398-00042003
CURRENT FILING DATE: 2003-03-17
PRIOR PHILOR DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR PHILNG DATE: 1997-06-06
PRIOR PHILNG DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                   Query Match 78.0%; Score 1917.5; DB 2 Best Local Similarity 77.0%; Pred. No. 2.3e-178; Matches 365; Conservative 41; Mismatches 45;
   EXPRESSING THEM (amended)
            FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/189, 977A
CURRENT PILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                    ORGANISM: Helicobacter pylori
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   TITLE OF INVENTION:
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LENGTH: 478
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                                                                                                                                                                                                                                                                     Length 478
                                                                                                                                                                               OTHER INFORMATION: H. pylori strain NCTC11639 (763)
OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
                                                                                                                                                                                                                                                                                                                 Indels
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Patent No. 639937
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
TILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1999-06-05
BARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PASELSE FASELSE FASELSE
SEQ ID NO 2
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US-09-092-315-2
                                                                                                                                 ORGANISM: Helicobacter pylori
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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Sequence 2, Application US/10189977A

Sequence 2, Application US/10189977A

Patent No. 6962806

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: PUCCESTC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: PUCCESTC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT APPLICATION NUMBER: US/09/733,524

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 2: 27

SEQ ID NO 2: 27

SEQ ID NO 2: 27

SEQ ID NO 2: 27
KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF 236
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Matches 361; Conservative
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Sequence 2, Application US/09733524A

Patent No. 6534296

GENERAL INPORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002

CURRENT PILLING DATE: 2000-12-07

PRIOR PILLING DATE: 1998-06-05

PRIOR PILLING DATE: 1998-06-05

PRIOR PILLING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 2

LENGTH: 486

LENGTH: 486
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|ABELISIDDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDD
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                                                  1 MFQPLLDAYIESASIEKITSKSPPPLKIAVANWW--GDEEVEEFKKNILYFILSQHYTIT
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                                   MFQPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII
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    31; Gaps
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    48; Indels
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   41; Mismatches
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ORGANISM: Helicobacter pylori
    361; Conservative
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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1 MFQPLLDAFIDSTHLDETTH.....TSFKIYRKAYQKSLPLLRAI
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GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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.09-733-524-17
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Perfect score:
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28 1737; 70.7 440 4 US:10-130-131-3 Sequence 3, Ap. 29 1737; 70.7 440 4 US:10-130-131-3 Sequence 3, Ap. 29 1737; 70.7 440 4 US:10-130-30-3 Sequence 3, Ap. 20 1737; 70.7 440 4 US:10-132-0-3 Sequence 3, Ap. 20 1737; 70.7 440 4 US:10-132-0-3 Sequence 3, Ap. 20 1731 S 69.9 445 4 US:10-132-0-3 Sequence 3, Ap. 20 1731 S 69.9 445 4 US:10-132-0-3 Sequence 3, Ap. 20 1731 S 69.9 445 4 US:10-132-0-3 Sequence 6, Ap. 20 1731 S 69.9 445 4 US:10-132-0-3 Sequence 6, Ap. 20 1731 S 69.9 445 4 US:10-132-0-3 Sequence 10, Ap. 1712 S 69.7 444 5 US:10-132-0-3 Sequence 11, Ap. 1712 S 69.7 444 5 US:10-130-13 Sequence 11, Ap. 1712 S 69.7 444 5 US:10-130-13 Sequence 11, Ap. 1712 S 69.9 445 4 US:10-130-13 Sequence 11, Ap. 1712 S 69.9 445 4 US:10-130-13 Sequence 11, Ap. 1712 S 69.9 471 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S Sequence 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S SEQUENCE 11, Ap. 1712 S US:10-744-11-2 S US:10-744-1	Sequence 3, Applia Sequence 3, Applia Sequence 3, Applia Sequence 18, Applia Sequence 6, Applia Sequence 6, Applia Sequence 12, Applia Sequence 16, Applia Sequence 16, Applia Sequence 13, Applia Sequence 13, Applia Sequence 13, Applia Sequence 13, Applia Sequence 25, Applia Sequence 25, Applia Sequence 25, Applia Sequence 25, Applia Sequence 25, Applia Sequence 25, Applia Sequence 26, Applia Sequence 26, Applia Sequence 26, Applia Sequence 27		fucosyltransferase fucosyltransferase  fucosyltransferase  5; Length 456;  7; Indels 0; Gaps 0;  9; Indels 0; Gaps 0;  NSEKKGFRDFILHFILKQRYKIILH 60  NSEKKGFRDFILHFILKQRYKIILH 60  NSEKKGFRDFILHFILKQRYKIILH 60  NEVPNFULFDYAIGFDELDFNDRYL 120
28 1737.5 29 1737.5 30 1737.5 31 1737.5 32 1722.5 33 1722.5 34 1718 34 1718.5 36 1718 36 1718.5 37 1712.5 39 1639 40 1558 41 1129 44 1129 44 1129 45 1075.5 5040ECC 20, PUBLICANT: APPLICANT: US-10-120-319-3 US-10-189-977-3 US-10-392-098-3 US-10-392-098-3 US-10-120-319-6 US-10-120-319-6 US-10-1392-098-6 US-10-764-212-12 US-10-764-212-6 US-10-764-212-6 US-10-764-212-6 US-10-764-212-6 US-10-764-212-6 US-10-764-212-6 US-10-764-212-8 US-10-764-212-8 US-10-764-212-8 US-10-764-212-8 US-10-764-212-8 US-10-764-212-25 US-10-764-212-25	ALIGNMENTS	164212  10  10  10  11  11  11  11  11  11	
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241 GYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHON 241 GYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQN 301 AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNEP 360

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               PUDLICATION NO. US20030166211A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE

FILE REFERRENCE: 20254/049001

CURRENT FILING DATE: 1909-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: US/09/092,315

PRIOR PLING DATE: 1997-06-06

PRIOR PLING DATE: 1997-06-06

WUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.7%; Score 1934.5; DB 4, Best Local Similarity 79.3%; Pred. No. 6.7e-152; Matches 365; Conservative 41; Mismatches 45;
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PRIOR APPLICATION NUMBER: US/09/733,524A
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Publication No. US20030166212A1
GENERAL INFORMATION:
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KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVRNTLGYKVKNKNEFLSQYKFNLCF
                                                             LVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRRDH
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Dengming
TITLE OF INVENTION ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
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                                                                                                                                      ERLLSKATPLLELSQNTSFKIYRKAYQKSLPLLRAI 456
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; Pred. No. 6.7e-152;
41; Mismatches 45;
                                                                                                                                                                            BRLLSKATPLLELSONTSFKIYRKAYOKSLPLLRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                   Sequence 1, Application US/10120319
Publication No. US20020164749A1
GENERAL INFORMATION:
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; ORGANISM: Helicobacter pylori
US-10-120-319-1
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Best Local Similarity 79.3%;
Matches 365; Conservative 4:
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LENGTH: 464
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FTCOSYLFRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-0499002
CURRENT APPLICATION NUMBER: US/10/392,098
CURRENT FILING DATE: 2003-03-17
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1 MFQPLLDAFIDSTHLDETTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII
                            1 MFQPILLDAYVESASIEKWASKSPPPIKIAVANWW--GDEBIKEFKNSVLYFILSQRYTIT
                                                                                         59 LHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR
                                                                                                                                                                                                                                                                           177 KRGFASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNBFLSQYKFNLCF
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ORGANISM: Helicobacter pylori fucosyltransferase
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Publication No. US20020164749A1
GENERAL INFORMATION:
                            FEATURE:

NAME/KEY:

LOCATION: (0)...(0)

OTHER INFORMATION: Strain 26695A
US-09-733-524-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                      Best Local Similarity 77.58
Matches 368; Conservative
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Sequence 15, Application US/09733524

Sequence 15, Application US/09733524

Sequence 15, Application US/09733524

GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM

FILE REPERENCE: 07254/049002

CURRENT APPLICATION NUMBER: 09/09/733,524

CURRENT FILING DATE: 1999-06-05

PRIOR PLILING DATE: 1999-06-06

PRIOR APPLICATION NUMBER: 60/048,857

PRIOR PLILING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 20

SOFTHARE: FREESE FREESE FREESE FREESE FREESE

LENGTH: 476
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                                                                                                                                                                                                                                                                                                                                                         9; Gaps
                                                                                                                                                                                                                                                                                                              DB 4; Length 464;
                                                                                                                                                                                                                                                                                                         Query Match 78.7%; Score 1934.5; DB 4; Length Best Local Similarity 79.3%; Pred. No. 6.7e-152; Matches 365; Conservative 41; Mismatches 45; Indels
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Helicobacter pylori
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58 ILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFND 117
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                                                         Gaps
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APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-PUCOSYLTRANFERASE
TITLE OF INVENTION: ALPHA-1, 3-PUCOSYLTRANFERASE
FILE REFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-06-05
PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PASCEQ for Windows Version 3.0
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                                                       24;
78.5%; Score 1929; DB 3; Length 476; 77.5%; Pred. No. 2e-151; tive 39; Mismatches 44; Indels 2
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us-10-764-212-20.rapbm

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FENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Helicobacter pylori
US-10-392-098-5
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                             58 ILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFND
                                            118 RYLRMPLYYAYLHYKAMLVNDTTSPYKLK--ALYTLKKPSHKFKENHPNLCALIHNESDP
                                                                                                                                            176 WKRGFASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNEFLSQYKFNLC
1 MFQPLLDAFIESASIEKMVSKSPPPPLKIAVANWW--GDEEIKEFKKSVLYFILSQRYAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
   APPLICANT: Taylor, Diane E.
   APPLICANT: Taylor, Diane E.
   APPLICANT: Ge, Zhongming
   TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
   FILE REFERENCE: 07254/04901
; CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/09/092,315
; PRIOR PPLING DATE: 1998-06-05
; PRIOR FILING DATE: 1999-06-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FRSISEQ for Windows Version 3.0
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; ORGANISM: Helicobacter pylori
US-10-189-977-5
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE APPLICATION NUMBER: US/0/392,098
CURRENT APPLICATION NUMBER: US/09/733,524A
PRIOR PLIING DATE: 2000-12-07
PRIOR PLLING DATE: 1990-06-05
PRIOR PLLING DATE: 1990-06-06
PRIOR PLLING DATE: 1990-06-06
NUMBER: PRESSING PRESSION NUMBER: US 60/048,857
PRIOR PLLING DATE: 1990-06-06
SOFTWARE: FREESEQ for Windows Version 4.0
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239 FENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYL
                                                                                HAHONAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHR
                                                                                                                 HTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFIF---YR
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LNEPLVIIDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRINYDDLRVNYDDLRVNYDDL 415
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Sequence 7, Application US/10120319;
Publication No. US20020164749A1
; FULL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: LALPHA-1, 3-PUCOSYLTRANFERASE
FILE REFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT FILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTESEQ for Windows Version 3.0
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; ORGANISM: Helicobacter pylori
US-10-120-319-7
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Best Local Similarity 77.23
Matches 366; Conservative
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LENGTH: 478
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; Sequence 7, Application US/10189977; Publication No. US20030166211A1

RESULT 10 US-10-189-977-7

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APPLICANT: The Governers of the University of Alberta, a Canada Corporation APPLICANT: Taylor, Diane B. APPLICANT: Taylor, Diane B. APPLICANT: Ge, Zhongming Taylor, Diane B. TITLE OF INVENTION: NUCLBIC ACIDS ENCODING ALPHA-1,3 TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: EXPRESSING THEM FILLS OF INVENTION: GARBER OF 107254/049002 CURRENT APPLICATION NUMBER: US/09/733,524 CURRENT PILLING DATE: 2000-12-14
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356 IARPLYTIDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRINYDDLRVNYDDL
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APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
PRIOR PLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,857
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US-10-189-977-7
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INFORMATION FOR SEQ ID NO: 8559
Query Match 78.0
Best Local Similarity 77.0
Matches 365; Conservative
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REPRENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/139,24A
PRIOR APPLICATION NUMBER: US/09/733,524A
PRIOR APPLICATION NUMBER: US/09/733,524A
PRIOR PLING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US/09/733,524A
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 7
***ENAMER: PSELSEQ for Windows Version 4.0
***SEQ ID NO 7
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                                                                                               ORGANISM: Helicobacter pylori fucosyltransferase
                                                                                                                                           78.2%; Score 1921.5; DB 79.1%; Pred. No. 9e-151; iive 41; Mismatches 4
 PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Publication No. US20030166212A1
GENERAL INFORMATION:
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, ORGANISM: Helicobacter pylori
US-10-392-098-7
                                                                                                                                                                           Conservative
                                                                                                                                                         Best Local Similarity
Matches 364; Conserv
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                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                KRGFASFVASNPNAPIRNAFYDALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MFQPLLDAFIDSTHLDBTTHK--PPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKII
                                                                                                          1 MFQPLLDAYVBSASIEKMASKSPPPLKIAVANWW--GDEEIKEFKNSVLYFILSQRYTIT
                                                                                                                                                                     THSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR
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                                             Gaps
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                           Indels
                                               45;
                       ; Pred. No. 1.8e-150; 41; Mismatches 45;
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FILING DATE: 17-DEC-1997
ATTORNEY AGENT INFORMATION:
NAME: MANDERS: AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COC
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
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US-10-764-212-6
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Sequence 17, Application US/09733524

Patent No. US20020068347A1

GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EVERSESING THEM

TITLE OF INVENTION: EVERSESING THEM

TITLE OF INVENTION: EXPRESSING THEM

TITLE OF INVENTION: UNMBER: US/09/733,524

CURRENT APPLICATION NUMBER: 05/092,315

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE FRANCE: DATE: 1997-06-06

SOFTWARE FRANCE: SALE FRANCE: 06/048,857

NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                            DB 4; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.6%; Score 1908.5; DB 4; Length Best Local Similarity 79.3%; Pred. No. 8.9e-150; Matches 363; Conservative 26; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 DHERLLSKATPLLELSQNTSPKIYRKAYQKSLPLLRAI 456
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                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...436
SEQUENCE DESCRIPTION: SEQ ID NO: 8559:
                                                                                                                                   ORGANISM: Helicobacter pylori
                LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       US-10-335-977-8559
                                                                                                                                                         FEATURE
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LENGTH: 479
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356 DLWEPLVTIDDLRVNYDDLRVNYDDLRINYDDLRVNYDDLRINYDDLRVNYDD
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US-10-764-212-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                             Length 479;
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Jeans Jeans
APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Neose Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Pucceyltransferases
FILE REFERENCE: 019957-019400US
CURRENT PAPLICATION NUMBER: US/10/764,212
CURRENT PILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 485
                                                                                                                                                                     77.2%; Score 1897; DB 3; 76.4%; Pred. No. 9.2e-149; tive 42; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.2%; Score 1897; DB 5; Best Local Similarity 75.4%; Pred. No. 9.3e-149; Matches 362; Conservative 41; Mismatches 47;
ORGANISM: Helicobacter pylori fucosyltransferase
                                           ); NAME/KEY: PEPTIDE

): LOCATION: (0)...(0)

; OTHER INFORMATION: Strain 763 from NCTC11639

US-09-733-524-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10764212
Publication No. US20050164338A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
FEATURE:
                                                                                                                                                                     Query Match
Best Local Similarity 76.49
Matches 363; Conservative
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2RYKII 58 	LDFNDR 118        LDFRDR 118	NESDPW 176       NESDPL 178	KFNLCF 236         KFNLCF 238	DYIRYLH 296  ::     DHVRYLH 298	SALHRD 356 :   YRD 355	406 VNYDDL 415	LPLLRA 455         LPLLRA 475	
. MFQPLLDAPIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDPILHFILKQRYKII 	IHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDR 	YLRMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNBSDPW	Y KRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF 	ENSQGYGYVTEKILDAYPSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAI	AHQNAYLDMLYENPINTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHY 	INBELVSVDDIRRDHDDLRVNYDDIRVNYDDLRVNYDDLRVNYDDLRVNY 	7DDLRRDHDDLRRDHERLLSKATPLLELSQNTSFKIYRKAYQKSLPLIRA      ::      :	
н н	59	119	177	237	297	357	407	
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Search completed: August 11, 2006, 19:53:03 Job time : 113.112 secs

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Sequence 284, App
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Sequence 5128, Ap
Sequence 5127, Ap
Sequence 4748, Ap
Sequence 4748, Ap
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5504, Ap
4624, Ap
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                                                                                        August 11, 2006, 19:47:49 ; Search time 17.3294 Seconds
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2458
1 MPQPLLDAPIDSTHLDBTTH.....TSPKIYRKAYQKSLPLLRAI
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-293-697-4788

US-10-449-902-44967

US-10-449-902-44967

US-10-537-642-21

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US-10-471-571A-5504

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US-10-471-571A-5608

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US-10-471-571A-508

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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                    Perfect score:
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123.5
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No.
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Sequence 34472, A	Sequence 11954, A	Sequence 23, Appl	Sequence 8, Appli	Sequence 9, Appli	Sequence 15, Appl	Sequence 80733, A	Sequence 80732, A	Sequence 80731, A	Sequence 3528, Ap	Sequence 3, Appli	Sequence 98565, A	Sequence 109804,	Sequence 98564, A	Sequence 109803,	Sequence 98563, A	Sequence 109802,	Sequence 18453, A	Sequence 6, Appli	Sequence 5, Appli	
US-10-953-349-34472	US-11-056-355B-11954	US-10-537-642-23	US-10-530-234-8	US-11-257-500-9	US-11-257-500-15	US-11-056-355B-80733	US-11-056-355B-80732	US-11-056-355B-80731	US-10-471-571A-3528	US-10-126-915-3	US-11-056-355B-98565	US-11-056-355B-109804	US-11-056-355B-98564	US-11-056-355B-109803	US-11-056-355B-98563	US-11-056-355B-109802	US-11-330-403-18453	US-10-537-642-6	US-10-537-642-5	
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3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	
97	97	97	96	95.5	95.5	95	95	92	94.5	94	94	94	94	94	94	94	93.5	93.5	93	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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APPLICANT: Dunas Mille Edwards, Jean Baptiste
APPLICANT: Dougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: JOBETT, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.U54.CIP
CURRENT TAPLICATION NUMBER: US/11/197,712
CURRENT APPLICATION NUMBER: US/09/876,997
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR PELING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR PELING DATE: 2000-03-06
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 YKLKALYTLKKPSHKFKENHPNLCALIHNES--DPWKRGFASFVASNPNAPIRNAFYDAL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYIEVDSYGECLRNKDLPQQLKNPASMDADGFYRIIAQYKFILAFENAVCDDYITEKFWR 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 NAIBPVASGGSVKN-TLGYKVKNK-----NEFLSQYKFNLCFENSQGYGYVTEKILD 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 AYFSHTIPIYWGSPSVAKDFNP--KSFVNVHDFNNFDEAIDYIRYLHAHQNAYLDMLYE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 EVLKSLRYL-VPLQSKNKLRKRLAPLVYVQSYCDP------PSDRDSYVR----ELM
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                  Sequence 284, Application US/11197712
Publication No. US20060130160A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: -31..-1
US-11-197-712-284
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US-11-197-712-284
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SEQ ID NO 284
LENGTH: 406
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCORDE THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 ENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNP--KSFVNVHDFNNFDEAIDYIRY 294
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Publication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A020FY1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-30

PRIOR PLLING DATE: 2003-05-30

PRIOR PLLING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 338;
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  -SFKALVD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 147.5; DB 6;
30.9%; Pred. No. 0.00012;
tive 30; Mismatches 57;
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  145 KRMKYLAANPAAYNQTLRWKYEGPSD--
                                                                                                                                  ; Sequence 5127, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Arabidopsis thaliana
US-10-953-349-5127
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SEQ ID NO 52598
LENGTH: 513
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT REPRENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                        DATACANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-15/9PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN PATENTION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 PLKLGVVPVYYGSPSIT-DWLPSNKSAILVSEFSHPRELASYIRRLDSD----DRLYE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 147.5; DB 6; Length 302; 30.9%; Pred. No. 9.9e-05; tive 30; Mismatches 57; Indels 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5128, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                              Sequence 5129, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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US-10-953-349-5128
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LENGTH: 323
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44967
    LENGIH: 246
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282 ENSNEEDYVTEKFFQSLVTGAIPVVIGAPNI-QEFSPGEGAILHIKELDDVPSIAKTAKR3 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNDRYLRMPLYYAYLHYKAMLVNDTT----SPYKLK---ALYTLKKPSH----KFKENHP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 NLCALIHNESD------PW------KRGFASFVASN--PNAPIRNAFYDA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNA------IEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFENSQGYGYVTEKI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 LQAHLKVDVYGRSHKPLPQGTMM------ETLSRYKFYLAFENSLHPDYITEKL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LDAYPSHTIPIYWGSPS---VAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQNAY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 WRNALEAW---AVPVVLG-PSRSNYERFLPPDAFIHVDDFQSPKDLARYLQELDKDHARY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44967, Application US/10449902

Publication No. US20060123505A1

GENERAL INPORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-AO25Y1-US

CURRENT APPLICATION NUMBER: 2003-05-29

PRIOR PLILNG DATE: 2003-05-30

PRIOR PLILNG DATE: 2002-05-30

PRIOR PLILNG DATE: 2002-05-30

PRIOR PRIOR PLILNG DATE: 2002-05-30

PRIOR SPLICATION NUMBER: JP 2002-383870

NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.3%; Score 131; DB 7; Length 336; 24.1%; Pred. No. 0.0028; ive 41; Mismatches 72; Indels
                                                                                             341 IASNQEAFNQSLRWKYDGPSD-----SFKALID 368
                                                                  295 LHAHQNAYLDML---YENPLNTIDGKAGFYQDLSFEKILD 331
                                                                                                                                                                                                                 Sequence 4748, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: H1-A0106
CURRENT PELLING DAITE: 2005-12-05
PRIOR APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     109 STNDNGKPHWWDHLHCAMSHYKFVLAIENTKTESYVTEKLFYALEAGSVPIYFGAPNVWD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 FIPPNSIIDASKESSLRELASYVKAVANDPVAYAEYHAWRRCGTL-GNFGRSREMSLDTL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 DFNPKSFVNVHDFNNFDEAIDYIRYLHAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    691 MSFINNKESSNINKDDVYNGNMDNHNHHVNNNNTLCNTSLSDLCSNNSSESKKQEAVCLN 750
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                                                                                                                                                                 20 GFEDI-------FIGYHAK-DDVQVTYAGKSFHT-SRSYHVSTEKRND-AL
                                                                                                                                 109 GFDELDFNDRYLRMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCAL
                                                                                                                                                                                                                                                      169 IHNES-----DPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVK
                                                                                                                                                                                                                                                                                                                                                                        --- FLSQYKFNLCFENSOGYGYVTEKILDAYFSHTIPIYWGSPSVAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 SNPNAPI-----RNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 GNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYLRMPLYYAYLHY
                                                                  51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10537642

Sequence 24, Application US/10537642

Publication No. US20060165719A1

GENERAL INFORMATION:

APPLICANT: Epimeune, Inc.

APPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Sette, Denise L.

APPLICANT: Carucci, Daniel J.

APPLICANT: Carucci, Daniel J.

APPLICANT: Suthwood, Scott

TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE

FILE REFERENCE: EPI-103X

CURRENT APPLICATION NUMBER: US/10/537,642

CURRENT FILING DATE: 2005-06-06

PRIOR APPLICATION NUMBER: US 60/431,494

MINIER OF STING DATE: 2005-12-06

MINIER OF STING DATE: 2005-12-06
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; Score 129.5; DB 6; Length 246; ; Pred. No. 0.0024; 45; Mismatches 89; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.0%; Score 123.5; DB 6; Best Local Similarity 19.0%; Pred. No. 0.13; Matches 79; Conservative 75; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Plasmodium falciparum
US-10-537-642-24
      5.3%;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 24
ENOTH: 1781
      Query Match
Best Local Similarity 22.9%
Matches 55; Conservative
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|: :: ||| :| || || 1964 AEYNQSHIEYISNYD----ELTNNSSY-IYNN 1915
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20.6%; Pred. No. 0.59;
ve 63; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/10537642
Publication No. US20060165719A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Plasmodium falciparum US-10-537-642-21
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Best Local Similarity 20.61
Matches 98; Conservative
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                                                                                                                445 AYQKS 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 YKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGFASFVASNPNA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 PIRNAFYDAL--NAIE-----PVASGGSVKNTLGYKVKNKNEFL--SQYKFNLCFEN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 SQCYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAH 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 QNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNI--LENDTIYHCNDAHYSALHRD 356
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                                                           849 NNTIFNKAVNEIMYSKEITN-------MANINRSSDEY---ITNANMENDANIM-NN 894
                                                                                                                                                         TIYHCNDAHYSALHRDLNEPLVSVDDLRRD---HDDLRVNYDDLRVNYDDL----RVNY 392
                                                                                                                                                                                                      NN--FDEAIDYIRYLHAHQNAYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILEND 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILHSNP--NEPSDLVFGNP 74
                                                                                                                                                                                                                                                                                                                                            | :| |:| |:| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :|
                                                                                                                                                                                                                                                                                                   DDLRVNYDDLRVNYDDLRRDHDDLRR----DHERLLSKATPLLELSQNTSFKIYRK 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Carucci, Denise J. APPLICANT: Sidney, John APPLICANT: Southwood, Scott APPLICANT: Southwood, Scott TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE FILE REPERENCE: EPI-103X
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CURRENT FILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: Patentin version 3.2
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Publication No. US20060165719A1
GENERAL INFORMATION:
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; ORGANISM: Plasmodium falciparum
US-10-537-642-10
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Best Local Similarity 19.6%;
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1053 YGILMNLTKKGKKDLRHLMHIINVFIKEISKLFDHDSLNKGINKYILDYYREKALITDVN 1112
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APPLICANT: Epimeune, Inc.
APPLICANT: Epimeune, Inc.
APPLICANT: Epimeune, Inc.
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Caruci, Daniel J.
APPLICANT: Caruci, Daniel J.
APPLICANT: Suthwood, Scott
TITE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
TILE REFERENCE: EPI-103X
CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOUTHARE: Patentin version 3.2
LENGTH: 2024
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726 RHAIFYKSEKRITTLLSELGKYSSENNSRIGESFTTY-YAIGKSENIYNILTLFSQNLFY
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APPLICANT:
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                                                                                                 APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Secretary of the Navy APPLICANT: Obolan, Deniel J. APPLICANT: Sidney, John APPLICANT: Sidney, John APPLICANT: Sidney, John APPLICANT: Sidney, John APPLICANT: Sidney, John APPLICANT: Suchwood, Scott TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE FILE REFRENCH: EPI-103X CURRENT APPLICATION NUMBER: US 60/431,494 PRIOR PILING DATE: 2002-12-06 PRIOR FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1161 SOFTWARE: PatentIn version 3.2 SEQ ID NO 9 IERNOTHER.
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4.7%; Score 116.5; DB 6; Length 2133;
Best Local Similarity 19.4%; Pred. No. 0.64;
Matches 93; Conservative 89; Mismatches 175; Indels 123;
                Sequence 9, Application US/10537642
Publication No. US20060165719A1
GENERAL INFORMATION:
APPLICANT: Epimmune, Inc.
APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
APPLICANT: Secretary of the Navy
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APPLICANT: The United States of America as Represented by the APPLICANT: Secretary of the Navy
APPLICANT: Sette, Alessandro
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Publication No. US20060165719A1
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ORGANISM: Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 -CALIHN------ESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVK 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 HSNPNEPSDLVFGNPLEQ---ARKILSYQNTKRVF---YTGENEVPNFNLFDYAIG--FD
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                                                     APPLICANT: Southwood, Scott
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
FILE REFERENCE: EPI-103X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2632, Application US/10471571A
Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2001-03-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR APPLICATION NUMBER: GB-0107661.1
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 2632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.5%; Score 111.5; DB 6; Length 1464; Best Local Similarity 21.0%; Pred. No. 0.99; Matches 90; Conservative 66; Mismatches 152; Indels 121;
                                                                                                                              CURRENT APPLICATION NUMBER: US/10/537,642
CURRENT FILING DATE: 2005-06-06
PRIOR APPLICATION NUMBER: US 60/431,494
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1161
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Plasmodium falciparum
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Carucci, Daniel J.
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994 MIQGDNDDM 1002
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US-10-471-571A-2632
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LENGTH: 1464
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                                                                                                                                                                                                        125 YYAYL----HY------KAMLVNDTTSPYKLKALYTLKKPSHKFKE--NHPNLCALIHN 171
                                                                                                                                                                                                                                                                                                                                172 ESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 S-----VAKDFNPKSFVN-VHDF----NNFDEAIDYIRYLHAHQNAYLDMLY--- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 ALHRDLNEPLVSVDDLRRDHDDLRV------NYDDLRVNYDDLRVNYDDLRVNY 399
                                                                                                                                                                                                                                                                                       44 DFILHFILKQRYKIILHSNPNEPSDLVFGNP------LEQA--RKILSYQNTK
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                                                             Query Match 4.5%; Score 111.5; LL C, Best Local Similarity 19.8%; Pred. No. 2; Conservative 78; Mismatches 157; Indels 171; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26-27W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SEQWIN99, version 1.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.5%; Score 111; DB 6; Length 554;
Best Local Similarity 18.5%; Pred. No. 0.27;
Matches 104; Conservative 85; Mismatches 180; Indels 194;
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; OTHER INFORMATION: alkaline phosphatase
US-10-471-571A-5504
; NAME/KEY: MISC_PEATURE
; LOCATION: (1)..(2397)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-2632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5504, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:
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ORGANISM: Staphylococcus aureus
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Gaps

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                                                                                                                                                                                                                                                                                                                                                     177 KRGFASFVASNPNA------PIRNAFYDALNAIEPVASGGSVKNTLGYKVK 221
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                                                 26 IIHASITYVLSEKHEQALATDARSYIYLVQDNEIDKVKKIVKQQNIDLLITKHDKKVFSS
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| Sequence 4624, Application US/10471571A
| Sequence 4624, Application US/10471571A
| Sequence 4624, Application US/10471571A
| Publication No. US200660115490A1
| GENERAL INFORMATION:
| APPLICANT: CHIRON SPA
| TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
| TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
| CURRENT APPLICATION NUMBER: US/10/471,571A
| CURRENT FILING DATE: 2003-09-12
| PRIOR PILING DATE: 2001-09-27
| NUMBER OF SEQ ID NOS: 5642
| SOFFWARE: SeqWin99, version 1.03
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4.5%; Score 110.5; DB 6; Length 1050;
Best Local Similarity 19.7%; Pred. No. 0.75;
Matches 107; Conservative 85; Mismatches 181; Indels 171;
                                                                                                                                                                                                                                                                     46 ILH----FILKQRYKIILHSNPNEPSDLVFGNPLEQARKILSYQN-
                                                                                                                 94 GE-NEVPNFNLFDYAIGPDELDFND-------
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; OTHER INFORMATION: hypothetical protein US-10-471-571A-4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NTSFKIYRKAYQK 448
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ORGANISM: Staphylococcus aureus
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LENGTH: 1050
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64NEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFN 102	103 LFDYAIGFDELDENDRYLRMPLYYAYLHYKAMLVNDTTSFY 143 	144 K	178 RGFASFTASNENAPIRNAFYDALNAIEPVASGGSVKNTILGYKV 220   :	221 KNKNEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNFKS 275	276 FVNVHDENNFDEAIDYIRYLHAHQNAYLDMLYENPLMTIDGKAGFYQDLSF 326 	127 EKILDFFRVILENDTIYHCNDAHYSALHRDLNEPLVSVDDLRRDHDDLRVNYDDLRVNYD 386	187 DLRVNYDDLRVNYDDLRVNYDDLRRDHBDLRRDHERLLSKATPLLELSQNTSFKIYRKAY 446 	147 QKSL 450  :    35 QQLL 598
175	103	144 3	355	221 1	276 1	327 1	387 1	595 (
oy Op	op ox	S S	SP 63	PP GA	ç Q	ç, Q	ç, qa	& a

Search completed: August 11, 2006, 19:54:01 Job time : 19.3294 secs

- protein search, using sw model OM protein Run on:

August 11, 2006, 19:53:30 ; Search time 118.313 Seconds (without alignments) 1723.552 Million cell updates/sec

US-10-764-212-16

Title: Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

2589679 seqs, 457216429 residues Searched:

Word size :

2589342 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

A\_Geneseq\_8:\* 1: geneseqp19 Database :

genesequ1980s:\* genesequ1990s:\* genesequ2000s:\* genesequ2001s:\* genesequ2001s:\* genesequ2003s:\* genesequ2003s:\* genesequ2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

SUMMARIES

	Description	70145 Hel	Aeb70205 H. pylori	Ë	Adj77816 Helicobac		_	Adj77810 Helicobac	Adj27345 Alpha-1,3	Aeb70131 Helicobac	Aeb70201 H. pylori	5 H.	N	Adj27347 Alpha-1,3	~	Abu52257 Helicobac	Abg30885 H. pylori		Adj27355 Alpha-1,3		Abg30884 H. pylori	He	Aeb70193 H. pylori	Aeb70204 H. pylori
COLUMNIA	ΩI	AEB70145	AEB70205	AEB70199	ADJ77816	ADJ27351	AEB70137	ADJ77810	ADJ27345	AEB70131	AEB70201	AEB70195	ADJ77812	ADJ27347	AEB70133	ABU52257	ABG30885	ADJ77820	ADJ27355	AEB70141	ABG30884	AEB70149	AEB70193	AEB70204
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de	Query Match	100.0	15.2	15.2	15.2	15.2	15.2	13.2	13.2	13.2	12.1	12.1	12.1	12.1	12.1	11.9	11.9	11.9	11.9	11.9	11.9	11.2	10.8	10.8
	Score		68	68	68	68	68	59	59	59	54	54	54	54	54	53	23	53	53	53	23	20	48	48
	Result No.		7	m	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

			He.	Abg30887 H. pylori Adj77818 Helicobac Adj27353 Alpha-1,3		н. не1 н.
9 AEB70203 9 AEB70197 5 ABG30882	8 ADJ77814 8 ADJ27349 9 AEB70135		2 AAW86008 5 ABG30881 5 ABG32639	5 ABG30887 8 ADJ77818 8 ADJ27353	9 AEB70206 3 AAB10737 5 AB1151565	9 AEB70202 5 ABU51720 9 AEB70154
246 377 485	4 4 4 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	169 171 545	464 501 49	40 90 40 40 40 40 40	32 32 32 32 32	247 146 227
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## ALIGNMENTS

Helicobacter pylori fucosyl transferase, PutB, protein, SEQ ID NO: 16. Fucosyltransferase; protein production; enzyme AEB70145 standard; protein; 446 AA. Helicobacter pylori; strain 1111. 06-OCT-2005 (first entry) AEB70145; 

/note= "Encoded by AG" 'note= "Encoded by GC" 'note= "Encoded by AG" /note= "Encoded by AG" Location/Qualifiers Key Misc-difference 168 Misc-difference 355 Misc-difference 435 Misc-difference 408

US2005164338-A1

28-JUL-2005.

22-JAN-2004; 2004US-00764212.

22-JAN-2004; 2004US-00764212.

(NEOS-) NEOSE TECHNOLOGIES INC. (UYAL-) UNIV ALBERTA.

Bezila DJ; Simala-Grant J, Taylor D, Johnson KF,

WPI; 2005-521417/53. N-PSDB; AEB70144.

New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.

Claim 1; SEQ ID NO 16; 97pp; English.

The present invention provides alpha-1,3/4-fucosyltransferase (also

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180 240 240 300

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termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKOFNPKEFVNVHDFNNFDEAIDYIKYLHTH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDBRLLQNASPLLEL 420
                                                                                                                                                                                                                                                                                                       61 ONPNBFSDLVFSNPLGSARKILSYQNAKRVFYTGENBVPNFNLFDYAIGFDBLDFRDRYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H. pylori fucosyl transferase, FutB, protein, ORF19C2B.pep SEQ ID NO: 76.
                                                                                                                                                                                                                                                                                                                                                                                                       121 RMPLYYDRIHHKAESVNDTTSPYKLKONSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEEIKEFKKSVLYFIFSQRYTIALH
                                                                                                                                                                                                                                                                                                                               61 QNPNBFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEPLSQYKFNLCFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTH
                                                                                                                                                                                                                                    1 MFQPLLDAYVESASIEKMASKSPPPLKIAVANWWGDEBIKEFKKSVLYFIFSQRYTIALH
                                                                                                                                                                                                                                                                                                                                                                             121 RMPLYYDRLEHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYBDLRVNYBRLLQNASPLLBL
                                                                                                                                                              DB 9; Length 446;
                                                                                                                                                                                                 0; Indels
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                                                                                                                                                              100.0%; Score 446; 100.0%; Pred. No. 0;
                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein; 247 AA
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                                                                                                                                                                                 Best Local Similarity
                                                                                                                               Sequence 446 AA;
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                                                                                                                The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymuclecides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase (amino acids 1-247)
                                                                                                                                                                                                                                                                                                                                                                                                             74 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                             New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                       73 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK
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                                                                                                                                                                                                                                                                                                                    Length 247;
                                                                                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Pred. No. 1.4e-57;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fucosyltransferase; protein production; enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson KF,
                                                                                   Disclosure; SEQ ID NO 76; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                  protein fragment.
                                                                                                                                                                                                                                                                                   Sequence 247 AA;
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                                                                                                                                                                                                                                                                                                                                                         68;
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73 NPLGSARKILSYQNAKRVPYTGENEVPNFNLPDYAIGFDELDFRDRYLRMPLYYDRLHHK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Futh and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to Neactylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to strain 1962 FutB protein sequence of the invention.
                                                                                         73 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK 132
                                                                                                        53 NPLGSARKILSYQNAKRVFYTGENEVPNFNLPDYAIGFDELDFRDRYLRMPLYYDRLHHK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide encoding fucosyltransferase protein, usefu for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                                                                                                             Futh, Futh, alpha 1-3/4 fucosyltransferase, glycoprotein, glycolipid, fucose, N-acetylglucosamine, glycoconjugate, enzyme.
                                                                  Gaps
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                                      15.2%; Score 68; DB 9; Length 256; 100.0%; Pred. No. 1.4e-57; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                     Helicobacter pylori strain 19C2 FutB protein SegID 8.
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                                                                                                                                                                                                                                        ADJ77816 standard; protein; 277 AA.
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                                                                                                                                                                                                                                                                                            (first entry)
                                                                 68; Conservative
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nes 68; Conserva
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                                                     Best Local Similarity
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              Sequence 256 AA;
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Matches 68
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74 NPLGSARKILSYQNAKRVPYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a subscrotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucosy residue from a donor substrate the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and acceptor substrate on glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-1,3/4-fucosyltransferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori; strain 19C2 FutB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 4; 84pp; English.
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                                                                                                  133 AESVNDTT 140
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134 AESVNDTT 141
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134 AESVNDTT 141
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Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fucosyl; fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004009793-A2
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RESULT 6 AEB70137

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Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Futh, Futh, alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                      Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.2%; Score 68; DB 9; Length 277; Best Local Similarity 100.0%; Pred. No. 1.5e-57; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori strain 1182 FutB protein SeqID 2.
                                                                                                                                                                                                                                                                                                                                              Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
                                                                                                                   Fucosyltransferase; protein production; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 8; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ77810 standard; protein; 486 AA.
AEB70137 standard; protein; 277 AA.
                                                                                                                                                 Helicobacter pylori; strain 19C2
                                                                                                                                                                                                                                                                                                    (NEOS-) NEOSE TECHNOLOGIES INC.
                                                                                                                                                                                                                                         22-JAN-2004; 2004US-00764212
                                                                                                                                                                                                                                                                      22-JAN-2004; 2004US-00764212
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                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AESVNDTT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AESVNDTT 141
                                                                                                                                                                                                                                                                                                                  UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-521417/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AEB70136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004009838-A2
                                                                                                                                                                               US2005164338-A1
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                                                           06-OCT-2005
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                          AEB70137;
                                                                                                                                                                                                                                                                                                                    (UYAL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
ADJ77810
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This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Puth and PutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to Neactylglucosamine), such that they are useful in the preparation of altocoyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 1182 FutB protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 DDLRVMYDDLRVMYDDLRVMYDDLRVMYDDLRVMYDDLRVMYBRLLLQNASPLLELSQNT 458
                                                                                                                                                                                                                              New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLBLSQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase; fucosyl; fucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
13.2%; Score 59; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori; strain 1182 FutB
                                                                                                                                                                                                                                                                                                  Claim 16; SEQ ID NO 2; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ27345 standard; protein; 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NEOS-) NEOSE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-1,3/4-fucosyltransferase.
                                                                                                               (NEOS-) NEOSE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                              23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2003; 2003WO-US023155.
                               23-JUL-2003; 2003WO-US023057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bezila DJ;
                                                                                                                                                  Bezila DJ
                                                                                                                                                                                 WPI; 2004-123401/12.
N-PSDB; ADJ77809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004009793-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson KF,
                                                                                                                                                  Johnson KF,
29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ27345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
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Sequence 486 AA;

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                                                                                             This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate to the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                       400 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated fucosyltransferase polynucleotides and polypeptides, useful
for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                              Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and acceptor substrate on glycoprotein.
                                                                                                                                                                                                                                                                             366 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT
                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori fucosyl transferase, FutB, protein, SEQ ID NO: 2.
                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                 13.2%; Score 59; DB 8; Length 486;
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bezila DJ;
                                                                                                                                                                                                                                           100.0%; Pred. No. 1.6e-48; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               production; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 2; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                       AEB70131 standard; protein; 486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori; strain 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEOS-) NEOSE TECHNOLOGIES INC
                                                                          Claim 1; Fig 1; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2-JAN-2004; 2004US-00764212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simala-Grant J, Taylor D,
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                       59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYAL-) UNIV ALBERTA
WPI; 2004-132958/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-521417/53.
N-PSDB; AEB70130.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fucosyltransferase;
                                                                                                                                                                                                                                             Similarity
           N-PSDB; ADJ27344
                                                                                                                                                                                                             Sequence 486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005164338-A1
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                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                           Best Local
Matches 5
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                                                                                                                                                                                                                                                                                                                                   RESULT
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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleofides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.

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                                                                                                                                                                                                                                                                                                                                                                                                  H. pylori fucosyl transferase, FutA, protein, 1111FutA.pep SEQ ID NO: 72.
                                                                                                                                                458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                           400 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLELSQNT
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                      366 DDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDFYLRMPLYY
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                Length 486;
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                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 54; DB 9; Length 245
100.0%; Pred. No. 6.6e-44;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bezila DJ
             Score 59; DB 9; I
Pred. No. 1.6e-48;
13.2%; Sco...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 72; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fucosyltransferase; protein production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori; strain 1111.
                                                                                                                                                                                                                                                              AEB70201 standard; protein; 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEOS-) NEOSE TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                          59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simala-Grant J, Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-521417/53.
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2005164338-A1
                                                                                                                                                                                                                                                                                                                                                      06-OCT-2005
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                                                                                                                                                                                                                                                                                                          AEB70201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                       Matches
                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          datches
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                                                                                                                                                                                                                                           AEB70201
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This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Putch and PutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 1111 FutA protein sequence of the invention.
                                                      New isolated polynucleotide encoding fucosyltransferase protein, usefu for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYY
                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 54; DB 100.0%; Pred. No. 1.1
                                                                                                                      Claim 16; SEQ ID NO 4; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bezila DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 2; 84pp;
            WPI; 2004-123401/12.
N-PSDB; ADJ77811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-132958/13.
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADJ27346
                                                                                                                                                                                                                                                                                                                                                                        Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fucosyl; fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004009793-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and mucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the sequence is Helicobacter pylori fucosyltransferase of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase catalytic domain (amino acids 27-417) protein fragment.
                                                                                                                                                                                                                                                                                                                         New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FutA, FutB; alpha 1-3/4 fucosyltransferase, glycoprotein, glycolipid, fucose, N-acetylglucosamine, glycoconjugate, enzyme.
H. pylori fucosyl transferase, FutA, protein fragment, SEQ ID NO: 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 54; DB 9; Length 391; 100.0%; Pred. No. 1e-43; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                              Bezila DJ;
                              Fucosyltransferase; protein production; enzyme
                                                                                                                                                                                                                                                                Simala-Grant J, Taylor D, Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 66; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ77812 standard; protein; 432 AA
                                                           Helicobacter pylori; strain 1111.
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2002US-0424894P.
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                                                                                                                                                      22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                    22-JAN-2004; 2004US-00764212.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004009838-A2
                                                                                           US2005164338-A1
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                                                                                                                        28-JUL-2005
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Gaps 126

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ö 1.le-43; DB 8;

Length 432; Indels

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This sequence represents an alpha-1,3/4-fucosyltransferase protein which
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                                 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
12 NPLGSARKILLSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDKYLRMPLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori; strain 1111 FutA.
                                                                                                                                                                                                                      ADJ27347 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-1,3/4-fucosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2003; 2003WO-US023155.
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ABU52257 standard, protein; 418 AA.

RESULT 15
ABUS2257
ID ABUS2

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Gaps

us-10-764-212-16.olig.rag

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synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated fucosyltransferase polynucleotides and polypeptides, useful
for synthesizing oligosaccharides, glycoproteins, or glycolipids.
               glycoprotein. The method involves contacting a recombinant through transferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 4.
 was used in the method of the invention for producing a fucosylated
                                                                                                                                                                                                                                                                                                   NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYY 125
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                                                                                                                                                                                                   12.1%; Score 54; DB 8; Length 432;
100.0%; Pred. No. 1.1e-43;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                 Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                                         Protein-protein interaction; ulcer; selected interacting domain; SID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                             Helicobacter pylori selected interacting domain (SID) protein #1601.
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent an illegible residue
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                                              07-MAY-2003 (first entry)
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Best Local Similarity 100.
Matches 53; Conservative
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(INSP ) INST PASTEUR
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                                                                                                                                            Helicobacter pylori
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              ABU52257;
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Search completed: August 11, 2006, 20:00:03 Job time : 118.313 secs

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Score 54; DB 9; Length 432; Pred. No. 1.1e-43;

12.1%; Scor. 100.0%; Pred. No. 1... 0; Mismatches

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Matches

NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYY

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.	sin - protein search, using sw model August 11, 2006, 20:00:25 ; Search time 20.9374 Seconds (without alignments)	US-10-764-212-16 score: 446 1 MFQPLLDAYVESASIEKMASKIYRKAYQKPIKNPY	ng table: OLIGO Gapop 60.0 , Gapext 60.0	hed: 283416 seqs, 96216763 residues	size: 1	number of hits satisfying chosen parameters: 283416	um DB seq length: 0 um DB seq length: 2000000000	processing: Listing first 45 summaries	e: PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES	Query Score Match Length DB ID Description	53 11.9 425 2 C64567 fucosyltransf	53 II.9 476 2 C646UI IUCOBYILTAN	46 . 10.3 454 2 B71914 a alpha (1,3)	9 2.0 667 2 T09482 ring f	8 1.8 318 2 T11260 NADH2 dehyd	8 1.8 559 2 B36307	8 1.8 1007 2 S48535	8 1.8 1139 2 B54962	8 1.8 1141 2 A54962 8 1.8 1409 1 OFFFFF	8 1.8 3343 2 S44887	7 1.6 71 2 B82791	7 1.6 79 2 T10336	7 1.6 139 2 P97095 integral	7 1.6 152 2 C97249	7 1.6 162 2 H97620 hypothetic	7 1.6 162 2 AG2843 conserved hyp	7 1.6 173 2 AC1000 Shikimate	7 1.6 173 2 AD0019 shikimate	7 1.6 174 2 G83712 nypotheti 7 1.6 215 2 E84078 hymotheti	7 1.6 219 2 AF1320 hypotheti	7 1 6 210 2 301602	7 1.6 219 2 AF1692 hypotheti	7 1.6 219 2 AF1692 7 1.6 222 2 G86717
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			228	8	C69859	two-component resp
	_		240	-4	A65134	shikimate kinase (
			240	~	H91157	shikimate kinase I
			240	~	F86003	shikimate kinase I
			244	~	296796	probable heat shoc
			267	8	T22978	hypothetical prote
			268	~	C90566	hypothetical prote
			290	0	T34443	
			304	~	D71290	
			319	~	AH3527	D-xylose-binding p
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			336	ď	H84767	probable peroxidas
42			341	~	G82014	dTDPglucose 4,6-de
			351	~	S07407	peroxidase (EC 1.1
			352		BVECHD	molybdenum transpo
45			352	7	AE0595	molybdenum.transpo
					ALIG	ALIGNMENTS
RESULT 1 C64567						
fucosyltransfe	rase -	Heli	cobac	ter	. pylori	fucosyltransferase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori	icobac	ter p	ylori		:	
C; Date: 09-Aug	1-1997	#sedn	ence	rev	rision 0:	C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C,Accession: C64567	164567		-		£	G and an an and the second sec
Filomo, U.F.; white, C.; Meriavage, A.K.; Craycon, Peterson, S.; Loftus, B.; Richardson, D.; Dodson,	Loftu	. n	Ric	har	dson, D	**Tillum, U.F.; Miller, O.; Activades, A.F.; Oldrey, R.; Khalak, H.G.; Glodek, A.; McKenne, Peterson, S.; Loftus, B.; Richardson, D.; Dodeson, R.; Khalak, H.G.; Glodek, A.; McKenne, P. B.; M. C
son, J.D.; Ke.	ley, J	. M.	Cotto	ď,	M.D.; W	son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997	9-547	1997			4	
A;Authors: Wa; A;Title: The c	lin, E	e qenc	уев, още в	¥.s ĭequ	ence of	A,Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference m	mber:	A6452	0, MT.	ĬĎ.	9739446.	A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64567	164567					
A;Status: preliminary; nucleic acid	iminar	y; nuc	cleic	ac	id seque	sequence not shown; translation not shown
A; morecure Lype: DNA A:Pesidies: 1-425 /TOM>	425 AT	Ž.				
A, Cross-refere	nces:	UNIPR	OT:02	514	2; UNIP	A,CYGSE-ZEFERENCES: UNIPROT:025142; UNIPARC:UPI00000D70CA; GB:AE000554; GB:AE000511; NID:
			;			
Query Match Best Local Similarity	imilar	itv	100.0%;	60	"	oore 53; lb 2; length 425; Pred. No. 1.2e-48;
Matches 53	53; Con	Conservative	tive		ö	matches 0; Indels 0; Gaps 0;

## 225 NKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277 RESULT 2 C64601 셤

224 NKSBFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276

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tucosyltransferase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004
C;Accession: C64601
S;Multe, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
San, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Pujli, C.; Bowman, C.; Watthey, L.
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A.
A;Attle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64601
A;Reference DNA
A;Reliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-476 <TOM>A;Residues: 1-476 <TOM>A;Residues: 1-476 <TOM>A;Residues: 1-476 <TOM>A;Cosse-references: UNIPROT:025366; UNIPARC:UP100000D70CB; GB:AE000578; GB:AE000511; NID: 224 NKSEFLSQYKFNLCPENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276 . 0 Query Match 11.9%; Score 53; DB 2; Length 476; Best Local Similarity 100.0%; Pred. No. 1.4e-48; Matches 53; Conservative 0; Mismatches 0; Indels ઠે

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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 100.0%; Pred. No. 0.6
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                          A;Map position: Xp22.3
C;Superfamily: rfp transforming protein
F;6-65/Domain: RING finger homology <RRN>
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                                                                                                                                                                A;Gene: FXY
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A;Cross-references: UNIPROT:Q9ZLI3; UNIPARC:UPI00000D3665; GB:AE001491; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: fucT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
G;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: B71914
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-436 <ARN>
A;Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UPI0000D36D2; GB:AE001528; GB:AE001439; NIC
A;Experimental source: strain J99
                                                                                                                                                                                                                     C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71862
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09482
E;Accession: T09482
E;Perry, J; Feather, S; Smith, A.; Palmer, S.; Ashworth, A.
Submitted to the EMBL Data Library, November 1997
A;Pescription: The human FXY maps to chromosome Xp22.3: Implications for evolution of A;Reference number: 216687
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225 NKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277
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                                                                                                                                                                                          alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 RNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 10.3%; Score 46; DB 2; Length 436; l Similarity 100.0%; Pred. No. 4.7e-41; 46; Conservative 0; Mismatches 0; Indels
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Matches 46; Conserv
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Matches
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A; Modecule type: mRNA
A; Residues: 1-667 < PER>
A; Cross-references: UNIPROT: 015344; UNIPARC: UPI000012F0E6; EMBL: AF035360; NID: g2827993; I
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T11260
R;Black IV, W.C.; Robhrdanz, R.L.
Mol. Biol. Evol. 15, 1772-1785, 1998
A;Title: Mitochondrial gene order is not conserved in arthropods: prostriate and metastri
A;Reference number: Z17252; MUID:99083443; PMID:9866211
A;Reference number: Z17252; MUID:99083443; PMID:9866211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alkaline phosphatase (BC 3.1.3.1) - rat
N'Alternate names: phytase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: Si8408; S1757 DeLuca, H.F.
B;Gtrom, M.; Krisinger, J.; DeLuca, H.F.
B;Chim: Bjophys. Acta 1090, 299-304, 1991
A;Title: Isolation of a mRNA that encodes a putative intestinal alkaline phosphatase regular feetence number: S18408; MUID:92062729; PMID:1954251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 [similarity] - hardbacked tick (Ixc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-318 <BLA>
A,Cross-references: UNIPROT:099805; UNIPARC:UPI0000976B1; EMBL:AF081828; NID:94164542;
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A; Residues: 1-551 «STR»
A; Residues: 1-551 «STR»
A; Residues: 1-551 «STR»
A; Cross-references: UNIPROT: P51740; UNIPARC: UPI0000132000
A; Cross-references: UNIPROT: P51740; UNIPARC: UPI0000132000
B; Cross-references: University R; Sano, S.; Masutani, H.; Nakagawa, H.
B; Vang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
B; Chim. B; Diophys: Acta 1075, 75-82, 1991
A; Title: Purification and characterization of phytase from rat intestinal mucosa.
A; Reference number: S17576; MUID: 91370007; PMID: 1654110
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C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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1.8%; Score 8; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Length 667;
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A; Molecule type: DNA
A; Residues: 1-1007 < VOS>
A; Cross -references: UNIDARC: UP10000133814; EMBL: Z75035; MIPS: YOR127w; NID: g1420329; PID: e
A; Experimental source: strain S288C
R; Wiemann, S.; Rechmann, S.; Benes, V.; Voss, H.; Schwager, C.; Vlcek, C.; Stegemann, J.;
Yeast 12, 281-288, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Cricefulus griseus (Chinese hamster)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: B54962
R;Yang, J; Sato, R; Goldstein, J.L.; Brown, M.S.
R;Tang, J; Sato, P. 1994
A;Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that that the A;Reference number: A54962; MUID:95047343; PMID:7958866
                                                                                                                                                                                                                                          A,Title: Sequencing and analysis of 51 kb on the right arm of chromosome XV from Sacchard A,Reference number: S63860; MUID:97060020; PMID:8904341
                                                                                                                                                                                                                                                                                                                                 sterol regulatory element binding protein 2 precursor - human
N;Alternate names: basic-helix-loop-helix-leucine zipper transcription factor SRBBP-2
C;Species: Homo sapiens (man)
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A,Molecule type: DNA
A,Residuca: 1-1007 <CHF>
A,Cross-references: UNIPARC:UP10000133814; GB:U07421; NID:g460972; PID:g460973
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F;13-66/Domain: LIM metal-binding repeat homology <LIM2>
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches
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ilarity 100.0%; Pred. No. 12;
Conservative 0; Mismatches
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   A; Reference number: S66965
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371 AIDYIKYL 378
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A;Molecule type: mRNA
A;Residues: 1-1139 <YAN>
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                 A; Accession: S63864
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                                   A;Accession: S67012
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A;Residues: 1-1007 (cTRS)
A;Cross-references: UNIPROT:P39083; UNIPARC:UPI0000133814; EMBL:U07421; NID:g460972; PIL
A;Cross-references: UNIPROT:P39083; UNIPARC:UPI0000133814; EMBL:U07421; NID:g460972; PIL
R;Miemann, S.; Rechmann, S.; Benes, V.; Voss, H.; Schwager, C.; Vlcek, C.; Stegemann, J.
submitted to the EMBL Data Library, August 1995
St. Description: Sequencing of 51 kilobases on the right arm of chromosome XV from S. cere
A;Recession: 860987
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A;Cross-references: UNIPARC:UP10000133814; EMBL:X94335; NID:g1262139; PID:e217748; PID:g
R;Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge, W.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              alkaline phosphatase (BC 3.1.3.1), intestinal - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 16-Aug-2004
C;Accession: B36307
R;Manes, T.; Glade, K.; Ziomek, C.A.; Millan, J.L.
Remais, T.; Glade, K.; Ziomek, C.A.; Millan, J.L.
A;Fitle: Genomic structure and comparison of mouse tissue-specific alkaline phosphatase
A;Reference number: A36307; MUID:91139124; PMID:2286375
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A;Residues: 1-1007 < WIE>
A;Gross-references: UNIPARC:UP10000133814; EMBL:X90518; NID:g1050808; PID:g1050813
A;Cross-references: UNIPARC:UP10000133814; EMBL:X90518; NID:g1050808; PID:g1050813
R;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia
B;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia
Bubmitted to the EMBL Data Library, December 1995
A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
A;Reference number: S61643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P24822; UNIPARC:UPI000002749A; GB:M61705; NID:g194048; PIDN:
C;Superfamily: Alkaline phosphatase
C;Keywords: intestine; phosphoprotein; phosphoric monoester hydrolase
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N;Alternate names: protein 03290; protein YOR127w; protein YOR3290w
C;Species: Saccharomyces cerevisian
C;Date: 02-Dec-1994 #sequence revision 02-Dec-1994 #text change 09-Jul-2004
C;Date: 02-Dec-1994 #sequence revision 02-Dec-1994 #text change 09-Jul-2004
C;Accession: $48535; $60987; $61683; $67012; $63864; JC6097
R;Chen, G; Zheng, L.; Chan, C.S.M.
A;Description: Molecular characterization of Dbm1, a novel rhoGAP protein in yeast.
A;Reference number: $48535
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                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches
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100.0%; Pred. No. 6.8
tive 0; Mismatches
A,Note: 10-Val was also found
C,Superfamily: Alkaline phosphatase
C,Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                312 PLNALDGK 319
                                                                                                                                                                                                                                                                                                          398 PLNALDGK 405
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A; Residues: 1-559 < MAN>
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Best Local S
Matches 8
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A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Stesidues: 1-71 < SINA
A;Cross-references: UNIPROT:Q9PFU3; UNIPARC:UPI00001368FF; GB:AE003903; GB:AE003849; NID:
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.S.; Bueno, M.R.P.; Camargo, L.B.A.; Carraro, D.M.; Carraro, D.M.; Carraro, D.M.; Carraro, D.M.; Fraga, J.S.; Frereita, A.J.S.
submitted to GenBank, June 2000
A;Mothors: Ferreita, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, M.L.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martinos, E.A;Authors: Martins, E.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Miraca, B.M.V.; Martinos, E.G.; Miyaki, C.Y.;
A;Authors: Martins, E.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Miraca, E.C.; Miyaki, C.Y.;
A;Authors: da Silva, A.C. R.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
A;Authors: da Silva, A.C. R.; da Silva, F.R.; da Silva, A.M.; Silva JT., W.A.; da Silvaire
A;Reference number: A59328
A;Reference number: A59328
A;Residues: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S44887
R;Du, Z.
Submitted to the EMBL Data Library, May 1993
submitted to the EMBL Data Library, May 1993
A;Pescription: Sequence of the C. elegans cosmid ZK112.
A;Reference number: S44887
A;Returus: preliminary
A;Returus: preliminary
A;Molecule type: DNA
A;Residues: 1-3343 <DUZ>
A;Cross-references: UNIPROT:P34616; UNIPARC:UPI000013BC7C; EMBL:L14324; NID:g289740; PID:
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C;Keywords: cytoskeleton; transmembrane protein
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C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                         Gaps
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                                                                                                       / Match 1.8%; Score 8; DB 1; Length 1409; Local Similarity 100.0%; Pred. No. 16; Conservative 0; Mismatches 0; Indels
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     F;271-433/Product: proteinase #status predicted <MAT3>
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100.0%; Pred. No. 37;
trive 0; Mismatches
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Matches 8; Conserv
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Matches
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N;Contains: copia protein, 31K; copia protein, 48K; proteinase
N;Contains: copia protein, 31K; copia protein, 48K; proteinase
C;Species: Drosophila melanogaster
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A03324; S03612; $\overline{8}$14835
Mol. Cell. Biol. 5, 1630-1638, 1985
A;Title: Complete nucleotide sequence of the Drosophila transposable element copia: home
A;Reference number: A03324; MUID:85267679; PMID:2410772
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A; Moseidues: 1-391,1375-1409 cMIL>
A; Cross-references: UNIPARC:UPIO00002A70E; EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:
A; Yoshioka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba, T.
R; Yoshioka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba, T.
Embo J. 9, 535-541, 1990
A; Title: Virus-like particle formation of Drosophila copia through autocatalytic process
A; Reference number: S14835; MUID:90151630; PMID:1689241
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A49397; A54962
R;Hua, X.; Yokoyama, C.; Wu, J.; Briggs, M.R.; Brown, M.S.; Goldstein, J.L.; Wang, X. Proc. Natl. Acad. Sci. U.S.A. 90, 11603-11607, 1993
A;Title: Second basic-helix-loop-helix-leucine zipper protein that stimulates A;Reference number: A49397; MUID:94089681; PMID:7903453
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A;Residues: 1-391,1375-1409 <YOS>
A;Cross-references: UNIPARC:UPI000002A70E; EMBL:X54147; NID:97749; PIDN:CAA38086.1; PID:
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A;Residues: 1-1409 <MOU>
A;Cross-references: UNIPROT:P04146; UNIPARC:UPI0000127EE3; GB:M11240; NID:g158615; PIDN:
R;Miller, K.; Rosenbaum, J.; Zbrzezna, V.; Pogo, A.O.
Nucleic Acids Res. 17, 2134, 1989
                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-1141 <HUA>
A;Cross-references: UNIPROT:Q12772; UNIPARC:UPI000003269D; GB:U02031; NID:g451329; PIDN:
A;Experimental source: HeLa cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: sequence extracted from NCBI backbone (NCBIP:140987)
R;Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A;Fitle: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A;Reference number: A54962; MUID:95047343; PMID:7958866
A;Contents: annotation
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C.Superfamily: sterol regulatory element binding protein
C.Keywords: DNA binding; membrane protein; transcription factor
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C;Superfamily: retrovirus-related polyprotein
C;Reywords: polyprotein; proteinas
P:2-433/Product: copia protein, 48K #status predicted <MAT1>
E;2-270/Product: copia protein, 31K #status predicted <MAT2>
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1.8%; Score 8; DB 2; 100.0%; Pred. No. 13; tive 0; Mismatches

Local Similarity 100. 290 AIDXIKYL 297 373 Aibyikyi 380

RESULT 12

Query Match Best Loc Matches

A;Gene: GDB:SREBF2; SREBP2 A;Cross-references: GDB:273625

A;Gene: FlyBase:copia A;Cross-references: FlyBase:FBgn0000349

A; Accession: S14835

A; Accession: S03612

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                                              Gaps
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Query Match 1.6%; Score 7; DB 2; Length 71; Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches 0; Indels
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39 IKEFKKS 45

36 IKEFKKS 42

T10336

hypothetical protein 67 - Orgyła pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyła pseudotsugata nuclear polyhedrosis virus, OphNPV
C;Species: le-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004
C;Accession: T10336
R;Ahrens, C.A.; Russell, R.R.; Punk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyła pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10336
A;Accession: T10336
A;Accession: T10336
A;Accession: J-79 - AHR.
A;Reidcule type: DNA
A;Reidcule type: DNA
A;Reidcule type: DNA
A;Cross-references: UNIPROT:010321; UNIPARC:UPI000006182F; EMBL:U75930; NID:g2934903; PI

0; Indels Query Match
1.6%; Score 7; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 249 EKILDAY 255

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Gaps

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Search completed: August 11, 2006, 20:09:17 Job time: 22.9374 secs 9 EKILDAY 15 g

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224 NXSEFISQYKFNLCFENSQGYQYVTEKILDAYPSHTIPIYWGSPSVAKDFNPK 276
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Best Local Similarity 100.0%; Pred. No. 5e-45;
Matches 53; Conservative 0; Mismatches 0; Indels
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PANTHER; PTHR11929; Glyco_trans_10; 1.
Complete proteome; Glycosplransferase; Transferase.
SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;
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                                                                 August 11, 2006, 19:54:19; Search time 157.197 Seconds (without alignments) 2624.463 Million cell updates/sec
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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025366_HELPY
025631_HELPY
026873_HELPY
020213_HELPY
020213_HELPY
020211_HELPY
042C08_9CAUD
042C08_9CAUD
040272_MUSCA
080272_MUSCA
TRI18_HUSCA
TRI18_HUSCA
TRI18_HUSCA
TRI18_HUSCA
081070_CARPL
090410_CARPL
098XF7_DROME
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                                           - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                          446
1 MFQPLLDAYVESASIEKMAS.
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                             US-10-764-212-16
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Q6hmv7 bacillus th Q8luk3 bacillus an Q7tsu8 mus musculu Q6rsw5 sus scrofa Q92329 pseudomonas Q9esr4 mus musculu Q9esr4 mus musculu Q9esr4 pseudomonas Q9405 ixodes hexa Q74403 anopheles q Q7441 anopheles q Q7441 helicobacte Q36jw3 marinobacte Q36jw3 marinobacte Q36jw3 marinobacte	8. A.A.	rewbl.	79; i). acteria; Campylobacterales;	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  TRAIN=26695 / ATCC 700392;  MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;  Tomb JF., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,  Fleischmann R.D., Ketchum K.A., Klenk HP., Gill S.R.,  Bougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,  Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,	D., Utterback T.R., Peterson J.D., T.P., Fujii C., Bowman C., Borodovsky M., Karp P.D., T., He gastric pathogen Helicobacter	e http://www.uniprot. tribution-NoDerivs Li. A.	A. fferase activity; IEA. activity, transferring glycosyl; IEA. oo acid glycosylation; IEA. ns_10.
Q6HWV7_BACHK Q81 LW3_BACAN Q91 LW3_BACAN Q91 SU8_BOUSE Q92 329_PSEPU Q92 SZA4_Q0SES Q92 SZA4_Q0SES Q92 Q98 Q5 LXCHE Q93 Q98 Q5 LXCHE Q93 Q6 Q13 Q6 Q13 Q6 Q13 Q6 Q13 Q6 Q13 Q6 Q13 Q6 Q13 Q6 Q13 Q6 Q13 Q13 Q13 Q13 Q13 Q13 Q13 Q13 Q13 Q13	ALIGNMENTS RT; 425	UniProtKB/TrEMBL 11.	ORFNames=HP_0379; 1obacter pylori). Epsilonproteobact acter.	DOI=10 R., Cl. lenk H. cenbush cdson D	1. J.F., Ut., Borode I.C.;		se act: vity, lid gly
Q6HMV7 Q71UK3 Q71UK3 Q6RSW8 Q9E3Z9 Q9E3Z4 Q9ESZ4 Q9EV16 Q8FV16 Q9B05 Q70FA1 Q3B3G6 Q70FA1	Δ.	o uniP on 1. 24.	RFNames obacter psilon cter.	SCALE ( 52185; vage A., A., Kl , Quach Richal	ayne J eidman s W.S., nter J ce of t	Consortium, ive Commons -; Genomic	IEA. ansfers se acti mino ac
000000000000000	RY;	int rei	py1	GE 92; r1a2 r1a X G. E.	Goc Goc Goc Goc Goc Goc Goc Goc Goc Goc	1 11 1 15	ne; ltr era n a
1186 1186 1186 122 133 133 133 135 135 135 135 135 135 135	PRELIMINARY;	integrated into Un sequence version 1 entry version 24.	nsferase. usNames=HP0379; er pylori (Camp Proteobacteria; eraceae; Helico	CC 7003 CC 7003 Pubmed O., Ke Ketchu elson K	Berg D.E., Gocayne J.I. Cotton M.D., Weidman Wallin B., Hayes W.S., Fraser C.M., Venter J.( e genome sequence of th	ighted by the Uniprot Considered under the Creative AE000511; AAD07447.1; -; 54567; C64567.	.6020; C:membrane; IEA. 18417; F:fucosyltransferase .6757; F:transferase activit 16486; P:protein amino acid IPR001503; Glyco_trans_10.
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	r 1 2 HBLPY 025142 HBLPY	025142; 01-JAN-1998, 01-JAN-1998, 07-FEB-2006,	Fucosyltransferase. OrderedLocusNames=HP_0379, ORDeredLocusNames=HP0379, ORDeredLocusNames=HP0379, ORDeredLocusNames=HP0379, Bacteria, Proteobacteria, Bacteria, Proteobacteria, Helicobacteraceae, Helicobacter. Intili	NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA STRAIN=26695 / ATCC 700392; MEDLINE=97394467; PubMed=925185; DOI=10.103 MEDLINE=97394467; PubMed=925185; DOI=10.103 MEDLINE=97394467; PubMed=925185; DOI=10.103 MEDLINE=97394467; PubMed=925185; DOI=10.103 MEDLINE=97394467; PubMed=925185; DOI=10.103 MEDLINE=9739467; PubMed=925185; DOI=10.103 MEDLINE=9739467; PubMed=9739467; ubMed=9739467; PubMed=973947; PubMe	y E.K y J.M ey L. H.O. compl		GO; GO:0016020; GO; GO:0008417; GO; GO:0016757; GO; GO:0006486; InterPro; IPR00
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EMBL, AY450598; AAR88433.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016021; E:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
GO; GO:0016757; F:transferase activity, transferase.
InterPro; IPR011929; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10; 1.
Glycosyltransferase; Transferase.
SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;
                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
"Molecular Cloning and Functional Expression of a Novel Helicobacter pylori {alpha}-1,4 Fucosyltransferase."; Glycobiology 15:1076-1083(2005).
                                                                                                                 Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 272
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                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 2; Le
Pred. No. 6.2e-42;
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100.0%; Pred. No. c...
0; Mismatches
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Best Local Similarity 100.0
Matches 50, Conservative
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GO; GO:0008417; P:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97394467; PubMed=9222185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Peleischmann R.D., Ketchum K.A., Klenk H.-F., Gill S.R.,
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
Glodek A., McKenney K., PitzGerald L.M., Lee N., Adams M.D.,
Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
Smith H.O., Praser C.M., Venter J.C.,
"The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10; Interpreter proteome; Glycosyltransferase; Transferase.
SEQUENCE 476 AA; 55927 WW; 32BFFDBBD36E1F74 CRC64;
                                                                                                                                                                                                                                                                                                         [1]
WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGST35_HELPY PRELIMINARY; PRT; 432 AA. QGST35; 05-UUL-2004, integrated into UniProtKB/TrEMBL 07-UUL-2004, sequence version 1. 07-FEB-2006, entry version 8.
                                                                                              01-JAN-1998, integrated into UniprotKB/TrEMBL. 01-JAN-1998, sequence version 1. 07-PEB-2006, entry version 25. 07-PEB-2006, entry version 25. OrderedLocusNames=HP0651; ORPNames=HP_0651;
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PubMed=16000696; DOI=10.1093/glycob/cwj004;
Rabbani S., Miksa V., Wipf B., Ernst B.;
                                                        476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000511; AAD07710.1; -; Genomic_DNAPIR; C64601; C64601.
                                                        PRT;
                                                                                                                                                                                                                                                            Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 388:539-547(1997).
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LinkHub; O25366; -.
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                                                    OZ5366_HELPY
O253667
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pylori.

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EMBL, AF194963; AAF35291.2; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0008417; F:fucansferase activity, transferring glycosyl. .; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.

Glycosyltransferase; Transferase.

Glycosyltransferase; Transferase.

SEQUENCE 462'AA; 54560 MW; BD27F8B351ECE752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniproc.org/Terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20138342; PubMed=10671538; DOI=10.1074/jbc.275.7.4988; Rasko D.A., Wang G., Palcic M.M., Taylor D.E.; "Cloning and characterization of the alpha(1,3/4) fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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                                                            01-0CT-2000, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 2.
07-FEB-2006, entry version 17.
Alpha-1,3/4-fucosyltransferase.
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Nature 397:176-180(1999).
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G9; G0:0016020; C:membrane; IEA.
G9; G0:00160417; F:fucosyltransferase activity; IEA.
G9; G0:0016/57; F:transferase activity, transferring glycosyl. . .; IEA.
G9; G0:0016/57; F:transferase activity, transferring glycosyl. . .; IEA.
G0; G0:0016/57; F:transferase activity, transferring glycosyl. . .; IEA.
G0; G0:0016/57; F:transferase activity, transferase.
FIRELISPS; F:transferase.
FIRELISPS; G1ycosyltransferase.
Complete proteome; G1ycosyltransferase; Transferase.
SEQUENCE 436 AA; 50699 MW; IDB2066AE98FA6IE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9921682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., Gelonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9921682; DOI=10.1038/16495,
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., delege B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                     Name-fucu; ORFNames-jhp 1002;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%; Score 46; DB 2; Length 436; 100.0%; Pred. No. 8.1e-38; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999, integrated into UniProtKB/TrEMBL. 01-MAY-1999, sequence version 1. 21-FEB-2006, entry version 23. ALPHA (1,3)-FUGOSYLTRANSFERASE. Name=fucT; ORFNames=jhp_0596; Helicobacter pylori J99 (Campylobacter pylori
                                                                                          01-MAY-1999, integrated into UniProtKB/TrEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001439; AAD06573.1; -; Genomic DNA
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                                                             PRT;
                                                                                                       01-MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA-(1,3)-FUCOSYLTRANSFERASE.
                                                                                                                                                                                                  Helicobacteraceae; Helicobacter,
NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacteraceae, Helicobacter.
                                                            Q9zkd7 helpj preliminary;
Q9zkd7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NCTC 11639;
MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;
Ge Z., Chan N.W.C., Palcic M.M., Taylor D.E.;
"Cloning and heterologous expression of an alphal,3-fucosyltransferase gene from the gastric pathogen Helicobacter pylori.";
J. Biol. Chem. 272:21357-21363(1997).
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
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EMBL; AE001439; AAD06169.1; -; Genomic_DNA.
PIR; B71914; B71914.
BioCyc; HPYL85963:JHP0596-MONOMER; -.
GO; GO:0016050; C:membrane; IRA.
GO; GO:0016417; F:fucosyltransferase activity; IEA.
GO; GO:0006417; F:fucosyltransferase activity; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
Interpro; IPR001503; Glyco_trans_10.
PANTHER; PTHR11929; Glyco_trans_10.
COMPLETE POTCHOME; Glyco_trans_10.
EANTHER; PTHR11929; Glyco_trans_10.
COMPLETE FORCEOME; Glycop_transferase; Transferase.
SEQUENCE 454 AA; 53448 MM; 3262687131263AB0 CRC64;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
PANTHER; PTHR1929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  Length 454;
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100.0%; Pred. No. 8.4e-38;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998, integrated into UniProtKB/TrEMBL
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07-FEB-2006, entry version 26.
Alphal,3-fucosyltransferase.
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Best Local Similarity
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20 RGVVSFVAS 28

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus macedonicus (Macedonian mouse).
Bukaryota; Metazoa; (Abrdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0; Montoya-Burgos J.I., Boursot P., Galtier N.; "Recombination explains isochores in mammalian genomes.";
                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                     PubMed=15788529; DOI=10.1073/pnas.0501140102;
Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
"The complete genomes and proteomes of 27 Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY954955; AAX91190.1; -; Genomic DNA.
SEQUENCE 34 AA; 4006 MW; 263AB27910DE2E16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          bacteriophages.";
Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.0%; Score 9; DB 2;
100.0%; Pred. No. 0.96;
ative 0; Mismatches
                                                                                                                        07-JUN-2005, integrated into UniProtKB/TrEMBL. 07-JUN-2005, sequence version 1. 07-FEB-2006, entry version 3.
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InterPro; IPR003879; Butyrophylin.
InterPro; IPR003877; SPRY_ropt.
Pfam; PF00622; SPRY; 1.
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SEQUENCE 94 AA; 10617 MW;
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These 9; Conservative
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04 zcus;
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GO; GO:0016020; C:membrane; IRA.
GO; GO:0008417; F:fucosyltransferase activity; IRA.
GO; GO:0016757; F:tucansferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016787; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016787; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:001678; F:transferase activity, transferring glycosyl. . .; IEA.
Glycosyltransferase; Transferase.
Glycosyltransferase; Transferase.
SEQUENCE 333 AA; 39154 MW; CFFCBIAC127E0A8C CRC64;
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                                                                                                                                                                                                                                                                                                                              Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
NCBI_TaxID=210;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=320839;
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PubMed=15788529; DOI=10.1073/pnas.0501140102;
Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
"The complete genomes and proteomes of 27 Staphylococcus aureus
                                                                                                                                                                                                                                     STRAIN=NCTC 11637;
MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
Martin S.L., Edbrooke M.R., Hodgman T.C., van den Eijnden D.H.,
Bird M.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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100.0%; Pred. No. 0.96;
tive 0; Mismatches 0; Indels
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SEQUENCE 34 AA; 3962 MW; 348D427904DF6E16 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
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01-JAN-1998, integrated into UniProtKB/TrEMBL. 01-JAN-1998, sequence version 1. 07-FEB-2006, entry version 23. Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-). Name=fucT;
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J. Biol. Chem. 272:21349-21356(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arvicola terrestris (Buropean water vole).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Gilres, Rodentia, Sciurognathi;
Muroidea, Cricetidae, Arvicolinae, Arvicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0; Montcya-Burgos J.I., Boursot P., Galtier N.; Recombination explains isochores in mammalian genomes."; Trends Genet. 19:128-130(2003).
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SEQUENCE 94 AA; 10617 MW; 1485630849C1B84F CRC64;
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100.0%; Pred. No. 2.4;
tive 0; Mismatches
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100.0%; Pred. No. 2.4;
tive 0; Mismatches
                                                          EMBL; AY181225; AAO62985.1; -; Genomic_DNA
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                                                                          Interpro, IPR001870, B302.
Interpro, IPR003879; Butyrophylin.
Interpro, IPR003877; SPRY_rcpt.
Pfam; PF00622; SPRY;
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Interpro; IPR003879; Butyrophylin.
Interpro; IPR003877; SPRY_rcpt.
Pfam; PP00622; SPRY; I.
PRINTS; PR01407; BUTYPHIANCDUF.
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Best Local Similarity 100.
Matches 9; Conservative
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Q80ZB5 MUSPL
D0 Q80ZB5-M
AC Q80ZB5,
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DT 01-JUN-20
DT 07-FEB-20
DE FXY (Frag
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Q80Z81_ARV
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                                                                                                                                                                                                                                                                                                                          Mus cervicolor (Fawn-colored mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Murinae; Mus.
                      Gaps
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MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
MONICOJA-Burgos J.I., Boursot P., Galtier N.;
"Recombination explains isochores in mammalian genomes.";
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mastomys.
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080275 MUSCE
D QB0275, MUSCE PRELIMINARY; PRT; 94 AA.
D QB0275, MUSCE PRELIMINARY; PRT; 94 AA.
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DF PXY protein (Fragment).
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100.0%; Pred. No. 2.4;
iive 0; Mismatches
    Pred. No. 2.4;
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InterPro; IPRO01870; B302.
InterPro; IPR003879; Butyrophylin.
InterPro; IPR003877; SPX_rcpt.
Pfam; PF00622; SPRY; 1.
                      0; Mismatches
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    100.08;
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Mus platythrix (Flat-haired mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                 STRAIN=PTX;
MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
MONICOY-BURGOD J.I., Boursot P., Galtier N.;
"Recombination explains isochores in mammalian genomes.";
Trends Genet. 19:128-130(2003).
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InterPro; IPR001870; B302.
InterPro; IPR001879; Butyrophylin.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHINCDUF.
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SEQÜENCE 94 AA; 10587 MW; 123565BEF9C7084F CRC64;
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Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches
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Search completed: August 11, 2006, 20:08:10 Job time : 159.197 secs

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/EMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/7_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/PCTUS_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/PCTUS_COMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/RCCOMB.pep:*/
/EMC_Celerra_SIDS3/ptodata/2/jaa/RCCOMB.pep:*/
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-189-978-2
US-10-189-9778-6
US-09-092-315-6
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US-09-092-315-1
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seq length: 200000000
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	5.5	36		US-10-189-977A-14		_
	4. c	36		US-10-392-098A-14	Sequence 14,	Appl
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	1.8	1141	-	US-08-668-123-54	Sequence 54	
				ALIGNMENTS		
RESULT 1						
Sequence 2, App	licatio	Application US/0909231	906	7315		
; Patent No. 6399337	337 TION:					
, APPLICANT: Taylor,	lor, D	Diane E.				
; APPLICANT: Ge,	Zhongming	ning				
; TITLE OF INVENTION: ALPHA-1,	TION	ALPHA-1		3-FUCOSYLTRANFERASE		
; FILE REFERENCE: 07254/049001	: 0725.	4 / 04 90C	<u>.</u>	315		
CORRENT AFFLIC	ALTON.	AFFLICATION NUMBER: US/	2	7,		
	ATTON 1	APPLICATION NIMBER:	Sign	5 60/048.857		
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; LENGTH: 486						
; TYPE: PRT	Tolochootlon	include rot	į			
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; Sequence 2, Applic	licatio	2, Application US/09733524A	973	3524A		
; Fatent No. 6534298	272					

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: G. Zhongming
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FURDESSION SYSTEMS FOR MAKING AND FITLE OF INVENTION: EXERRESSION THEM (amended)
FILLE OF INVENTION: EXERRESING THEM (amended)
FILLE OF INVENTION: EXERRESING THEM (amended)
FILLE OF INVENTION: EXERRESING THEM (amended)
FILLE OF INVENTION: EXERRESING THEM (amended)
FILLE OF INVENTION: EXERRESING THEM (amended)
FILLE OF INVENTION: UNMBER: US/09/733,524A
CURRENT FILLING DATE: 1998-06-05
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR FILLING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASKSEQ FOR WINDOWS VERSION 4.0

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APPLICANT: TAYLOT, Diane B.
APPLICANT: TAYLOT, Diane B.
APPLICANT: TAYLOT, Diane B.
APPLICANT: TAYLOT, DIANE
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: 0.254-0.4900.2
CURRENT APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR PLILING DATE: 2000-12-07
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: US/09/048,857
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 486
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Best Local Similarity 100.0%; Pred. No. 4.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels
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13.2%; Score 59; DB 2; Length 486;
Best Local Similarity 100.0%; Pred. No. 4.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongmin G.
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1.3 Fucosyltransferase;
FILE REPERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/1292,098A;
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR APPLICATION NUMBER: US 06/048,857
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR PLILNG DATE: 2000-12-07
NUMBER OF SEQ 1D NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10189977A Patent No. 6962806 GENERAL INPORMATION:
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Patent No. 7029891
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-2
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US-10-189-977A-2
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patent No. 6534296

general No. 6534296

general INPORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: WICKLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: BAPRESSING THEM (amended)

TITLE OF INVENTION: BAPRESSING THEM (amended)

TITLE OF INVENTION: BAPRESSING THEM (amended)

FILING DATE: 1000-12-07

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR APPLICATION NUMBER: US 60/048,857

PRIOR APPLICATION NUMBER: US 60/048,857

PRIOR APPLICATION NUMBER: US 60/048,857

SOFTWARE PEACENCE

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                            ; OTHER INFORMATION: H. pylori strain UA1182
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-2
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APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/04901
CURRENT PELLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
RAMLIER APPLICATION NUMBER: US 60/048,857
EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRAESEQ for Windows Version 3.0
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ilarity 100.0%; Pred. No. 2.3e-42;
Conservative 0; Mismatches 0;
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13.2%; Score 59; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 4.6e-48;
Matches 59; Conservative 0; Mismatches 0;
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; ORGANISM: Helicobacter pylori
US-09-733-524A-6
                      LENGTH: 486
TYPE: PRT
ORGANISM: Helicobacter pylori
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ORGANISM: Helicobacter pylori
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Best Local Similarity
Matches 53; Conserv
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Length 425; Indels

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OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
                                                                               Query Match
11.9%; Score 53; DB 3; Lo
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 53; Conservative 0; Mismatches 0;
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  11.9%; Score 53; DB 2; Length 425; 100.0%; Pred. No. 2.3e-42; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                   PATENTIAN NO. 6962806
GENERAL INFORMATION:
APPLICANT: Taylor. Diane E.
APPLICANT: Taylor. Diane E.
APPLICANT: Taylor. Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1, 3
TITLE OF INVENTION: REXPESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: 2002-03-07
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/189,977A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/09/733,524
FRIOR APPLICATION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR APPLICATION NUMBER: US 60/048,857
SPROR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Ge, Zhongming
APPLICANT: Ge, Zhongming
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase;
TITLE NET INVENTION: Alpha-1,3 Fucosyltransferase;
FILE REFERENCE: 017398-00042008
CURRENT FILING DATE: 2003-03-17
FRIOR PLLING DATE: 2002-04-09
FRIOR PLLING DATE: 2002-04-09
FRIOR PLLING DATE: 1997-06-06
FRIOR FILING DATE: 1997-06-06
FRIOR FILING DATE: 1997-06-05
FRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARCHING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARCHING DATE: 2010-12-07
SOFTWARE: PARCHING DATE: 2010-12-07
SOFTWARE: PARCHING DATE: 2010-12-07
SOFTWARE: PARCHING DATE: 221
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                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10189977A Patent No. 6962806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10392098A
Patent No. 7029891
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ORGANISM: Helicobacter pylori
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ORGANISM: Helicobacter pylori
                                                         53; Conservative
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                           Best Local Similarity
Matches 53; Conserva
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Best Local Similarity
Matches 53; Conserva
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     Query Match
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: TAYLOR, Diane E.

APPLICANT: TAYLOR, Diane E.

APPLICANT: TAYLOR, DIANE E.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US 09/092,315

FRIOR PILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-05

PRIOR PILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SEQ ID NOS: 27

FROM THE PARTICATION NUMBER: US 06/048,857

SEQ ID NOS: 27

SEQ ID NOS: 27

FROM THE PARTICATION NUMBER: US 06/048,857
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Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 53; Conservative 0; Mismatches 0; Indels
                                                                                                               GENERAL INCORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge. Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT APPLICATION NUMBER: US 60/048,857
EARLIER APPLICATION NUMBER: US 60/048,857
FARLIER FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRESSEQ FOR WINGOWS VERSION 3.0
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11.9%; Score 53; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 53; Conservative 0; Mismatches 0;
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; Sequence 5, Application US/09733524A
; Patent No. 6534298
RESULT 9
US-09-092-315-5
'Sequence 5, Application US/09092315
'Patent No. 6399337
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; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-1
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, ORGANISM: Helicobacter pylori
US-09-092-315-13
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LENGTH: 464
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FREERL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: WUCKELC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT FILING DATE: 2002-03-07

PRIOR PILING DATE: 2000-12-07

PRIOR PLING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

FRIOR PLING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 27

SOFFWARE: PASESEQ for Windows Version 4.0
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225 NKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 277
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) OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpPucT)

US-10-392-098A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1, 3 Fucosyltransferase;
FILE REPERENCE: 017398-000420US
CURRENT FILING DATE: 2003-03-17
PRIOR PLLING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 2003-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN OF SEQ ID NOS: 30
SOFTWARE: PATENTIN OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10392098A
Patent No. 7029891
GENERAL INFORMATION:
                                                                                                                 Sequence 5, Application US/10189977A
Patent No. 6962806
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ORGANISM: Helicobacter pylori
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Best Local Similarity 100.
Matches 53; Conservative
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Best Local Similarity
Matches 53; Conserva
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LENGTH: 476
TYPE: PRT
                                                                  RESULT 11
US-10-189-977A-5
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224 NKSEPLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.6%; Score 43; DB 2; Length 372
Best Local Similarity 100.0%; Pred. No. 8e-33;
Matches 43; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: GE, Zhongming
TITLE OF INVENTION: ALFHA-1, 3-FUCOSYLTRANFERASE;
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT APPLICATION NUMBER: US 60/048,857
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1. Application US/09092315
; Sequence 1. Application US/09092315
; Patent No. 6399337
; GENERAL INFORMATION:
; APPLICANT: Caylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
; CURRENT FILING DATE: 1998-06-05
; CURRENT FILING DATE: 1998-06-05
; EARLIER PILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6554298
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
                                                                                                                                                                       US-09-092-315-13
; Sequence 13, Application US/09092315
; Patent No. 6399337
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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; TITLE OF INVENTION: EXPRESSING THEM (amended)
; TITLE OF INVENTION NUMBER: US/09/733,524A
; CURRENT APPLICATION NUMBER: US 09/092,315
; PRIOR APPLICATION NUMBER: US 09/092,315
; PRIOR PLILING DATE: 1988-06-05
; PRIOR PLILING DATE: 1989-06-06
; PRIOR PLILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PASISEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-1
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Search completed: August 11, 2006, 20:10:51 Job time : 31.9076 secs

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Gaps ö

Query Match
9.6%; Score 43; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 9.6e-33;
Matches 43; Conservative 0; Mismatches 0; Indels

1 MPOPLLDAYVESASIEKMASKSPPPLKIAVANWMGDEEIKEFK 43

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241 SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNNFDEAIDYIKYLHTH 300
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US-10-764-212-72
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US-10-120-319-6
US-10-120-319-6
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Publication No. US20050164338A1
GENERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Roose Technologies, Inc.
APPLICANT: Neose Technologies, Inc.
APPLICANT: Neose Technologies, Inc.
APPLICANT: Overnors of the University of Alberta
TITLE OP INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OP SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
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US-10-35-977-8559

US-10-10-764-212-61

US-10-120-319-13

US-10-120-319-1

US-10-120-319-1

US-10-139-977-1

US-10-392-098-1

US-10-392-098-1

US-10-392-098-1

US-10-392-098-1

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US-10-392-098-1

US-10-120-319-8

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APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
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APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
                                                                                                                                                                                              421 SQNTSFKIYRKAYQKPIKNPYPYCAP 446
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Publication No. US20050164338A1
GRNERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
                                                                                                                                                                                                                                                                                                                        Sequence 76, Application US/10764212
Publication No. US20050164338A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Simala-Grant, Joanne
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TYPE: PRT
ORGANISM: Helicobacter pylori
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SEQ ID NO 76
LENGTH: 247
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US-10-764-212-70
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; OTHER INFORMATION: H. pylori strain 19C2 FutB fucosyltransferase; OTHER INFORMATION: catalytic domain conserved region positions 22-277 US-10-764-212-70
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APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REPERRICE: 07254/04901
CURRENT FILLING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR PILLING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 22
SUPTWARE: FARESE FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FARESE FILING DATE: 1997-06-06
SEQ ID NOS: 22
SOFTWARE: FARESE FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: H. pylori strain 19C2 FutB fucosyltransferase US-10-764-212-8
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APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Johnson, Karl F.
APPLICANT: Neose Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REPERENCE: 019957-019400US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
                                                                                                                Query Match
15.2%; Score 68; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 2.7e-57;
Matches 68; Conservative 0; Mismatches 0;
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15.2%; Score 68; DB 5; Lu
Best Local Similarity 100.0%; Pred. No. 2.9e-57;
Matches 68; Conservative 0; Mismatches 0;
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Publication No. US20020164749A1
GENERAL INFORMATION:
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US-10-764-212-8
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US-10-764-212-72
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LENGTH: 486
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Query Match
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
TITLE OF INVENTION: NUCLEIT ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REPRENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/392,098
CURRENT PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-06
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
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; Bequence 2. Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPEA-1, 3-FUCOSYLTRANFERASE
; FILE REPERENCE: 07254/049001
; CURRENT PELLING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US/10/189, 977
; PRIOR PELLING DATE: 1998-06-05
; PRIOR FILING DATE: 1998-06-05
; RIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FRAELSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-2
                                                                                                            Query Match
13.2%; Score 59; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 2.8e-48;
Matches 59; Conservative 0; Mismatches 0;
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                     ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-2
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; ORGANISM: Helicobacter pylori
US-10-392-098-2
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Matches 59; Conserv
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LENGTH: 486
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US-10-764-212-72
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APPLICANT: Johnson, Karl F.
APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Pucosyltransferases
FILE REPRENCE: 019957-019400US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Governors of the University of Alberta
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
13.2%; Score 59; DB 4; L. 100.0%; Pred. No. 2.8e-48; tive 0; Mismatches 0;
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Publication No. US20050164338A1
GENERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10764212
Publication No. US20050164338A1
GENERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
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ORGANISM: Helicobacter pylori
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                                                             59; Conservative
                           Best Local Similarity
Matches 59; Conserv
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US-09-733-524-16
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12 NPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYLRMPLYY 125
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US-10-764-212-4
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100.0%; Pred. No. 1.7e-43;
ive 0; Mismatches 0; Indels
                                                                                                                     Taylor, Diane

Jericant: Taylor, Diane

Johnson, Karl F.

APPLICANT: Bezila, Daniel James

APPLICANT: Bezila, Daniel James

APPLICANT: Governors of the University of Alberta

TITLE OF INVENTION: H. Pylori Fucesyltransferases

FILE REFERENCE: 01997-019400US

CURRENT APPLICATION NUMBER: US/10/764,212

CURRENT PILING DATE: 2004-01-22

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 66

LENGTH: 391
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APPLICANT: Taylor, Diane
APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Recaf Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10764212
Publication No. US20050164338A1
GENERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Helicobacter pylori
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Matches 54; Conservative
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Matches 54; Conserva
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LENGTH: 432
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GENERAL INFORMATION:
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM
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CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTEEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 53; Conservative 0; Mismatches 0; Indels
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Publication No. US20020164749A1
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming,
ATITLE OP INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
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11.9%; Score 53; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.7e-4
Matches 53; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/99/733,524
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1999-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 20
SOPTWARE: PastSEQ for Windows Version 4.0
Sequence 16, Application US/09733524
Patent No. US20020068347A1
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LOCATION: (0)...(0)
OTHER INFORMATION: Strain 26695B
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Sequence 6, Application US/10392098

Sequence 6, Application US/10392098

Publication No. US20030166212A1

GENERAL INFORMATION:

APPLICANT: Taylor, Diane B.

APPLICANT: Taylor, Diane B.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1, 3

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE OF INVENTION: EXPRESSING THEM (amended)

CURRENT APPLICATION NUMBER: US/09/733,524A

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR PILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 6

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                   Sequence 6, Application US/10189977
Publication No. US20030166211A1
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALFRA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 2002-07-03
FRICH APPLICATION NUMBER: US/09/092,315
FRICH FILING DATE: 1998-06-05
FRICH RILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Helicobacter pylori
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; ORGANISM: Helicobacter pylori
US-10-392-098-6
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Best Local Similarity
US-10-189-977-6
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US-10-392-098-6
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Search completed: August 11, 2006, 20:16:20 Job time : 108.678 secs

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Sequence 250, Application US/11289102

Bublication No. US20060121511A1

GENERAL INFORMATION:
APPLICANT: Lee, Hear M.
APPLICANT: Clark, Edwin
TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
FILE REFERENCE: 10338 NP
CURRENT APPLICATION NUMBER: US/11/289,102
CURRENT PILING DATE: 2004-11-39
PRIOR PILING DATE: 2004-11-30

NUMBER OF SEQ ID NOS: 395
SOFTWARE: Patentin version 3.3
LENGIH: 667
180 RGVVSFVAS 188
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US-10-471-571A-98
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Sequence 250, App
Sequence 24876, A
Sequence 24875, A
Sequence 3784, Ap
Sequence 30485, A
Sequence 34075, A
Sequence 34075, A
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63938, A
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117223,
106366,
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1771.230 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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                                                                                              August 11, 2006, 20:11:06; Search time 16.9493 Seconds
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             GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-953-349-24876

US-10-953-349-6784

US-11-056-355B-30485

US-11-056-355B-34780

US-11-056-355B-105984

US-11-056-355B-105984

US-11-056-355B-105984

US-11-056-355B-10505

US-11-056-355B-10505

US-11-056-355B-10505

US-11-056-355B-10505

US-11-056-355B-105036

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                                                                    - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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17428, Ap
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Publication No. US20060115490A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION SPAPE.
CURRENT PILING DATE: 2003-99-12

PRIOR PILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 5642

SOFTWARE: Seqwin99, version 1.03

SEQ ID NO 98

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Mo. 0.066;
0; Indels
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US-11-056-355B-8709

US-11-056-355B-87742

US-11-056-355B-17428

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US-11-056-355B-8572

US-11-056-355B-8572

US-11-056-355B-69280

US-10-953-349-31462

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100.0%; Pred. No. 0.0
Live 0; Mismatches
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Matches 9; Conservative
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APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FITLE OF INVENTION: BROONDED THERBY
FILE REPERENCE: 2750-1579 PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 6784
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Sequence 30485.

Publication No. US20060150283A1

Sequence 30485.

Publication No. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Brover, Vyacheslav

APPLICANT: Brover, Vyacheslav

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2004-02-13

PRIOR APPLICATION NUMBER: 60/544,190

FRIOR APPLICATION NUMBER: 60/544,190

SRQ ID NO 30485

LENGTH: 161
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APPLICANT: BIOVER, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUSZ
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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100.0%; Pred. No. 33;
ative 0; Mismatches
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100.0%; Pred. No. 33;
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; OTHER INFORMATION: Ceres Seq. ID no. 13497623
US-11-056-355B-30485
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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ORGANISM: Arabidopsis thaliana
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US-10-953-349-6784
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Best Local Similarity 100...
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Matches 7; Conservative
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    GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: 105/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 24876
LENGTH: 149
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FILE REPERENCE: 2750-1579-98042
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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                                                                                               Length 667;
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                                                                                                                                              0; Indels
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Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches
                                                                                                  DB 7;
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                                                                                               Query Match 2.0%; Score 9; DB 7
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   US-10-953-349-24876
Sequence 24876, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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Publication No. US20060107345A1
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                                                                                                                                                                                                                                           616 AFYDALNSI 624
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-250
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ORGANISM: Glycine max
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US-10-953-349-6784
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1.6%; Score 7; DB 7;
100.0%; Pred. No. 33;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches
                     ; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 13618494
US-11-056-355B-105984
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; LOCATION: (1)..(248)
; CTHEN INFORMATION: Ceres Seq. ID no. 13619377
US-11.056-355B-106366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: peptide
; LOCATION: (1)...(161)
; OTHER INDORMATION: Ceres Seq. ID no. 13618494
US-11-056-355B-117223
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
                                                                                    Query Match
Best Local Similarity 100.v.
7; Conservative
                                                                                                                                                                                                      69 LVPSNPL 75
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NAME/KEY: peptide
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## Sequence 43780.

## Sequence 43780.

## Sequence 43780.

## Sequence 43780.

## Sequence 43780.

## Sequence 10 No. U82066150283A1

## Sequence 10 No. U82066150283A1

## Sequence 10 No. U820661503A1

## TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

## TITLE OF INVENTION: Polypeptides Encoded Thereby

## TITLE OF INVENTION: Polypeptides Encoded Thereby

## TITLE OF INVENTION: Polypeptides Encoded Thereby

## CURRENT APPLICATION NUMBER: US/11/056,355B

## CURRENT FILING DATE: 2005-02-14

## PRIOR FILING DATE: 2004-02-13

## NUMBER OF SEQ ID NOS: 119966

## SEG ID NO 43780

** LENGTH: 161
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APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
RRIOR APPLICATION NUMBER: 60/544,190
RRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 105984
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100.0%; Pred. No. 33;
tive 0; Mismatches
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                                                                                    | FEATURE:
| NAME/KEY: peptide
| LOCATION: (1)...(161)
| OTHER INFORMATION: Ceres Seq. ID no. 13497623
| US-11-056-355B-34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: peptide; LOCATION: (1)..(161); OTHER INFORMATION: Ceres Seq. ID no. 13497623 US-11-056-355B-43780
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                                          TYPE: prt
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
FEATURE:
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 100.
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SEQ ID NO 34075
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APPLICANT: Brover,
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERENCE: 2750-12500-125
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 106366
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT PPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 11723
LENGTH: 161
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Length 161;
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUG2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 117605
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US-11-056-355B-106365
# Sequence 106365, Application US/11056355B
# Sequence 106365, Application US/11056355B
# Publication No. US20060150283A1
# GENERAL INFORMATION:
# APPLICANT: Brover, Vyacheslav
# TITLE OF INVENTION: Polypeptides Encoded Thereby
# TITLE OF INVENTION: Polypeptides Encoded Thereby
# PILE REFERENCE: 2750-1590PUS2
# CURRENT APPLICATION NUMBER: US/11/056,355B
# CURRENT FILING DATE: 2005-02-14
# PRIOR FILING DATE: 2004-02-13
# NUMBER OF SEQ ID NOS: 119966
# SEG ID NO 106365
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  1.6%; Score 7; DB 7; Length 248; 100.0%; Pred. No. 49; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 55;
tive 0; Mismatches
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| LOCATION: (1)..(277)
| OTHER INPORMATION: Ceres Seq. ID no. 13619376
| US-11-056-355B-106365
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; OTHER INFORMATION: Ceres Seq. ID no. 13619377
US-11-056-3558-117605
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Matches 7; Conservative
Query Match 1.6
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Sequence 27635, Application US/10953349
Publication No. US2006107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROW Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT PELLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27635
LIENGTH: 293
Sequence 117644, Application US/11056355B
; Sequence 117644, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; TITLE OF INVENTION: VOMBER: US/11/056,355B
; CURRENT APPLICATION NUMBER: 60/544,190
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR APPLICATION NUMBER: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 117604
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 55;
ative 0; Mismatches
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ORGANISM: Arabidopsis thaliana
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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#### ALIGNMENTS

New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids. Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 18. Bezila DJ; Fucosyltransferase; protein production; enzyme Johnson KF, "TTT Location/Qualifiers /note= "Encoded by AEB70147 standard; protein; 440 AA Helicobacter pylori; strain 802 (NEOS-) NEOSE TECHNOLOGIES INC (UYAL-) UNIV ALBERTA. 22-JAN-2004; 2004US-00764212 22-JAN-2004; 2004US-00764212 Simala-Grant J, Taylor D, (first entry) WPI; 2005-521417/53. N-PSDB; AEB70146. Misc-difference US2005164338-A1 06-OCT-2005 28-JUL-2005. AEB70147; 

The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproceins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.

Claim 1; SEQ ID NO 18; 97pp; English.

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421 YHKSLPLLRAIRRWVKKLGL 440
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                                                                                               61 NEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYLRMP
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sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
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                                            Gaps
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                          Length 440;
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                                  ; Pred. No. 0;
0; Mismatches
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                           100.0%; Score 440; 100.0%; Pred. No. 0
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                                    Best Local Similarity ivv. Matches 440; Conservative
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                                   Local Similarity
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          Sequence 440 AA;
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The invention relates a purified transmembrane segment-free alpha 1,3-

tucosyltransferase polypepide, having a repeat of the sequence: X 1-X 2-

Leu-Arg-X.3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Ash, and X 3 is

Leu-Arg-Man. Also included are the nucleic acid encoding the protein

(including its complement or fragment), a vector containing the nucleic

acid, a host cell containing uncleic acid or vector, an antibody which

conditing transmembrane segment-free alphal, 3- fucosyltransferase,

comprising a host cell modified with the nucleic acid or its

producing transmembrane segment-free alphal, 3- fucosyltransferase,

comprising a host cell modified with the nucleic acid or its

comprising the produced oligosaccharides, such as Lex, Ley or Elex, by

contacting the produced oligosaccharides, or by culturing the cell,

contacting the bost cell with a substrate, to produce oligosaccharides

contacting the obtained oligosaccharides. The nucleic acid is useful

as probe for detecting the nucleic acid, by contacting a sample with a

contacting the nucleic acid using polymerase chain reaction (PCR). The

contacting the nucleic acid using polymerase chain reaction (PCR). The

mullifying the nucleic acid using polymerase chain reaction (PCR).

contacting the nucleic acid using polymerase chain reaction (PCR).

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contacting the nucleic acid using polymerase chain reaction (PCR).

contacting the producing a transmembrane segment-free alphal, 3-

fucosyltransferase-funsion producing a transmembrane segment-free alphal, 3-

conceptle under conditions which allow expression and secretion of the

contacting the producing a lange way probe in a main and a series of the protein in a sample. The antibody is also useful for diagnosing disorders

conditioning disease, and for inhibiting abnormal applal, 3-

cucosyltransferase gene product activity. The nucleic acid using

the protein or cell are useful in the development of assays to detect

conditioning and p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEPSDLVFGSPIGAARKILSYQNTKRVFYAGENEVPNFNLFDYAIGFDELDLRDRYLRMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPFVFYRDLNEPLVSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Claim 6; Fig 6; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 440 AA;
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standardise OS field)

Sequence 454 AA;

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Enzyme, fucT; alphal, 3 fucosyltransferase; oligosaccharide, Lex; Ley;
sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                            H. pylori alphal, 3 fucosyltransferase #7.
                                         ABG30887 standard; protein; 454 AA
                                                                                                                                Helicobacter pylori; strain 11637.
421 YHKSLPLLRAIRRWVKKLGL 440
                                                                                                                                                                                                                                                                      Example 3; Fig 6; 37pp; English
                                                                                                                                                                                        98US-00092315.
                                                                                                                                                                          07-DEC-2000; 2000US-00733524.
                                                                      (revised)
(first entry)
                                                                                                                                                                                                      (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                   WPI; 2002-582480/62.
                                                                                                                                                                                                                    raylor DE, Ge Z;
                                                                                                                                              US2002068347-A1.
                                                                                                                                                                                        05-JUN-1998;
                                                                      29-AUG-2003
21-OCT-2002
                                                                                                                                                            06-JUN-2002
                                                         ABG30887;
                                    ABG30887
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The invention relates a purified transmembrane segment-free alpha 1,3the convertion relates a purified transmembrane segment-free alpha 1,3the convertion for transferase polypeptide, having a repeat of the sequence: X 1-X 2teu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is App or Am; and X 3 is

Ite, Val or Ala. Also included are the nucleic acid encoding the protein

C (including its complement or fragment), a vector containing the mucleic

acid, a host cell containing nucleic acid or test selectively binds to the protein and a gene expression system for

selectively binds to the protein and a gene expression system for

comprising transmembrane segment-free alphal, 3- fucosyltransferase,

comprising transmembrane segment-free alphal, 3- fucosyltransferase

comprising the protein with a substrate, to produce of slex, by

contacting the protein with a substrate, to produce oligosaccharides

con purifying the obtained oligosaccharides. The nucleic acid is useful

contacting the best cell with a substrate, to produce oligosaccharides

a probe for detecting the nucleic acid, by contacting a sample with a

nucleic acid probe that hybridises to alphal, 3-fucosyltransferase

and purifying the nucleic acid using polymerase chain reaction (PCR). The

contacting the mucleic acid using polymerase chain reaction of the

nucleic acid probe that hybridises to alphal, 3-fucosyltransferase

contacting the mucleic acid using polymerase chain reaction of the

contacting the mucleic acid using polymerase chain reaction of the

contacting the protein in a sample free presence of the protein in the

contacting the protein in a sample. The presence of the protein in the

contacting the protein in a sample free presence of the protein in the

contacting the protein in a sample free for diagnosing disorders

and monitoring disease, and for inhibiting abnormal alphal, 3
contacting the protein in a sample free for diagnosing contacting the protein or call are useful in the development of sasays to detect

contacting the protein in

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Lierniya of Ala. Also included are the nucleic acid encoding the protein (including its complement or fragment), a vector containing the nucleic acid, an entibody which acid, a host cell containing nucleic acid or vector, an antibody which selectively binds to the protein and a gene expression system for producing transmembrane segment-free alphal, 3- fucosyltransferase, comprising a host cell modified with the nucleic acid or its enzymatically active portion. The protein and cells are useful for producing fucosylated oligosaccharides, such as Lex, Ley or slex, by contacting the protein with a substrate, to produce oligosaccharides and purifying the protein with a substrate, to produce oligosaccharides and purifying the obtained oligosaccharides. The nucleic acid is useful as a probe for detecting the nucleic acid, by contacting a sample with a nucleic acid probe that hybridisation of the probe; or by polynucleotide, and detecting hybridisation of the probe; or by only nucleotide, and detecting hybridisation of the probe; or by charmed acid using polymerase chain reaction (PCR). The nucleic acid using polymerase chain reaction (PCR). The chost cell is useful for producing a transmembrane segment-free alphal, 3-fucosyltransferase-fusion protein, by growing the host cell containing a vector operably linked to a polynucleotide encoding a desired polypeptide or peptide under conditions which allow expression and secretion of the fusion protein in a sample. The presence of the protein in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2-Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is Ile, Val or Ala. Also included are the nucleic acid encoding the protein
                                                                                                            227 EFLSQYKFULCFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 284
                                                                                      224 EFLSQYKFNLCFENSQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzyme, fucT, alphal,3 fucosyltransferase, oligosaccharide, Lex; Ley;
sLex; Helicobacter pylori infection, malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates a purified transmembrane segment-free alpha 1,3-
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
  Length 454;
             le-48;
13.2%; Score 58; DB 5;
100.0%; Pred. No. 1e-48;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                H. pylori alphal, 3 fucosyltransferase #4.
                                                                                                                                                                                                                                           ABG30884 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori; strain 26695A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 6; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2000; 2000US-00733524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00092315
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                           58; Conservative
                                                                                                                                                                                                                                                                                                                                   (revised)
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                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-582480/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ge Z;
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                                                                                                                                                                                                                                                                                                                               29-AUG-2003
21-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor DE,
                                                                                                                                                                                                                                                                                      ABG30884;
  Query Match
                                             Matches
                                                                                                                                                                                                RESULT 4
ABG30884
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sample is indicative of infection by Helicobacter pylori or the presence of malignant cells. The antibody is also useful for diagnosing disease and for inhibiting abnormal alphal, 3-fucosyltransferase gene product activity. The nucleic acid is useful as part of ribozyme and/or triple helix sequences and for alphal, 3-fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alphal, 3 fucosyltransferase encdoed by the fucT gene. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-1,3-fucosyltransferase; fucT gene; Lewis X; Lewis Y; sialyl Lewis X; tumour associated antigen; cancer; infection; mucosal disease; diagnosis; fucosylated oligosaccharide.
                                                                                                                                                                Length 476;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori alpha-1,3-fucosyltransferase.
                                                                                                                                                                Query Match 12.5%; Score 55; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-45;
Matches 55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Asn is N-glycosylated"
332. .334
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341. .343
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435. .437 /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96. .99
/note= "Asn is N-glycosylated"
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/note= "peptide repeat"
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/note= "peptide repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "peptide repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "peptide repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori; strain NCTC 11639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                   AAW86008 standard; protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= 392. .39
                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                         Sequence 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                    17-0CT-2003
29-MAR-1999
                                                                                                                                                                                                                                                                                                                            AAW86008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                         AAW86008
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98WO-CA000564.

05-JUN-1998;

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This is the amino acid sequence of the novel alpha-1,3-
fucosyltransferase of Helicobacter pylori NCTC 11639, as deduced from the
newly isolated furg gene (see AAV8021). The enzyme is characterised by 8
c-terminal heptad repeats and by the lack of a transmembrane domain. The
absence of a transmembrane domain allows the enzyme to be readily
released from recombinant host cells. The enzyme to be readily
production of fucosylated oligosaccharides such as Lewis X, Lewis Y and
sialyl Lewis X, which are structurally similar to certain tumour
associated antigens found in mammals. These glycoconjugates also have
mammalian tumours. The enzyme can also be used to raise specific
antibodies. Inhibition of abnormal fucr gene product activity can be used
for the treatment of intestinal mucosal disease. (Updated on 17-OCT-2003
to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzyme; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley; sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                New isolated alpha-1-3-fucosyltransferase gene - obtained from
Helicobacter pylori, used to develop products for the diagnosis and
treatment of intestinal mucosal diseases, e.g. tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 52; DB 2; Length 464
100.0%; Pred. No. 1e-42;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori alphal, 3 fucosyltransferase #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG30886 standard; protein; 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori; strain 763.
                                                                                                                                                                                                                  Claim 6; Fig 2; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2000; 2000US-00733524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00092315.
97US-0048857P
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 52; Conservative
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                                (UYAL-) UNIV ALBERTA
                                                                                                WPI; 1999-059913/05.
N-PSDB; AAV80321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ge Z;
                                                                 Ge Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002068347-A1
16-JUN-1997;
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21-OCT-2002.
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                                                                 raylor DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG30886;
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Labigne A;

De Reuse H,

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The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                   complexes of protein-protein interactions in Helicobacter pylori, tul for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 51; DB 5; Length 130
100.0%; Pred. No. 3.3e-42;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                     Claim 6; Page 292; 642pp; English.
                                       Colland F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colland F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent an illegible residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001WO-EP015428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JAN-2001; 2001US-0259302P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-2003 (first entry)
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYBR-) HYBRIGENICS.
(INSP ) INST PASTEUR
                                       Rain J,
                                                                              WPI: 2002-674910/72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-674910/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori
                                                                                                                                                                            ulcers in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABX67002.
                                                                                                N-PSDB; ABX66254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200266501-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002
                                         Legrain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU52257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of malignant cells. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alphai, and monitoring disease, and for inhibiting abnormal alphai, and for inhibiting abnormal alphai, a part of ribozyme and/or triple helix sequences and for alphai, a fucosyltransferase gene regulation. Oligosaccharides synthesised using the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alphai, fucosyltransferase encoded by the fuct gene. (Updated on 29-AUG-2003 to
                                                         The invention relates a purified transmembrane segment-free alpha 1,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein-protein interaction; ulcer; selected interacting domain; SID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori selected interacting domain (SID) protein #853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 QCYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 52; DB 5; Length 479; 100.0%; Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU51509 standard; protein; 130 AA
                    Example 3; Pig 6; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 479 AA;
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Query Match Local Matches

ABU51509

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Gaps

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Length 130;

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New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                       Protein-protein interaction; ulcer; selected interacting domain; SID.
                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a complex of protein-protein interactions in
                                                                Helicobacter pylori selected interacting domain (SID) protein #1601.
                                                                                                                                                                                                                                                              Labigne A;
                                                                                                                                                                                                                                                              De Reuse H,
ABU52257 standard; protein; 418 AA.
                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 479; 642pp; English.
                                                                                                                                                                                                                                                                                                                                             ulcers in mammals.
          CXSXLLLXBXXBXBXBXBXBXSXXXXXCXCXCXXXCXXCXX
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28-DEC-2001; 2001WO-EP015428. 02-JAN-2001; 2001US-0259302P.

9-AUG-2002

(HYBR-) HYBRIGENICS

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Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for secening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                represent an illegible residue
         886666666666888
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Sequence 418 AA;

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                               Gaps
                                                           293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 343
                                                                                290 YLHTHPWAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 340
                               ö
11.6%; Score 51; DB 5; Length 418; 100.0%; Pred. No. 9.3e-42;
                           0; Indels
         100.0%; Preu.
                               51; Conservative
              Best Local Similarity
 Query Match
                               Matches
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H. pylori alphal, 3 fucosyltransferase #5. ABG30885 standard; protein; 424 AA (first entry) (revised) 21-OCT-2002 29-AUG-2003 ABG30885; RESULT 9 ABG30885 

Enzyme; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley; sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.

Helicobacter pylori; strain 26695B

US2002068347-A1

06-JUN-2002

07-DEC-2000; 2000US-00733524.

98US-00092315. 05-JUN-1998;

(UYAL-) UNIV ALBERTA

Ge Z; raylor DE, "PI; 2002-582480/62.

Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.

Example 3; Fig 6; 37pp; English.

The invention relates a purified transmembrane segment-free alpha 1,3fucosyltransferase polypeptide, having a repeat of the sequence: X 1-X 2fucustylx 3.4. Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
lea. May 3. A 4. Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
lea. May 1 or Ala. Also included are the mucleic acid encoding the protein
(including its complement or fragment), a vector containing the nucleic
acid, a host cell containing nucleic acid or vector, an antibody which
acid, a host cell containing nucleic acid or vector, an antibody which
acid, a host cell modified with the nucleic acid or its
comprising a host cell modified with the nucleic acid or its
comprising a host cell modified with the nucleic acid or its
contacting the protein with a substrate such as LacNAc-R and GDP-fucose,
and purifying the produced oligosaccharides, or by culturing the cell,
contacting the host cell with a substrate, to produce oligosaccharides
and purifying the obtained oligosaccharides. The nucleic acid is useful
as a probe for detecting the nucleic acid, by contacting a sample with a

This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes firth and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired

New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.

WPI; 2004-123401/12. N-PSDB; ADJ77819.

Claim 12; SEQ ID NO 12; 72pp; English.

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nucleic acid probe that hybridises to alphal, 3-fucosyltransferase
polynucleotide, and detecting hybridisation of the probe; or by
amplifying the nucleic acid unaing polymerase chain reaction (PCR). The
host cell is useful for producing a transmembrane segment-free alphal, 3-
fucosyltransferase-fusion protein, by growing the host cell containing a
ceftor operably linked to a polynucleotide encoding a desired polypeptide
or peptide under conditions which allow expression and secretion of the
fusion protein and isolating the fusion protein. The antibody is useful
cor peptide the protein in a sample. The presence of the protein in the
sample is indicative of infection by Helicobacter pylori or the presence
of malignant cells. The antibody is also useful for diagnosing disorders
and monitoring disease, and for inhibiting abnormal alphal, 3-
fucosyltransferase gene product activity. The nucleic acid is useful as
part of ribozyme and/or triple helix sequences and for alphal, 3-
the protein or cell are useful in the development of assays to detect
mammalian tumours. The present sequence represents an H. Pylori alphal, 3-
choosyltransferase encent sequence represents an H. Pylori alphal, 3-
choosyltransferase enchoos by the fuct gene. (Updated on 29-NUG-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Futh, Futh, alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
fucose, N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 YLHTHPNAYLDMLYENPLMTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 343
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 51; DB 5; Le
100.0%; Pred. No. 9.4e-42;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004 (first entry)
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Best Local Similarity 100.0
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                            standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 424 AA;
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NO: 12

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New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
    293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 343
                          297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDISFKKILDFFKTILENDTIYH 347
                                                                                                                                                                                                                                                                                      Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID
                                                                                                                                                                                                                                                                                                                              Fucosyltransferase; protein production; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simala-Grant J, Taylor D, Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 12; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU51153 standard; protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori; strain 26695.
                                                                                                                                                        AEB70141 standard; protein; 425
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                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100.0
Matches 51, Conservative
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N-PSDB; AEB70140.
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                                                                                                                                                                                                                                                                                                                                                                                                                      US2005164338-A1
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                                                                                                                                                                                                   AEB70141;
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                                                                                                                RESULT 12
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                                                                                                                                  AEB70141
ID AEB7
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oligosaccharide moieties (i.e. by transfer of a fucose residue to Nacetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, and encrymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 26695 FutA protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated glycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate to the glycoprotein. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and acceptor substrate on glycoprotein.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
                                                                                                                                                                                                                                                                                                                                293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 343
                                                                                                                                                                                                                                                                                                                                                         297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 347
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                                                                                                                                                                                                                                           11.6%; Score 51; DB 8; Length 425; 100.0%; Pred. No. 9.5e-42; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori; strain 26695FutA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   producing fucosylated glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ27355 standard; protein; 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-1,3/4-fucosyltransferase.
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2002US-0424894P.
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                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 51, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-132958/13.
N-PSDB; ADJ27354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fucosyl; fucose
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Best Local Si
Matches 51;
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RESULT 11 ADJ2735

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Bezila DJ;

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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein-protein interaction; ulcer; selected interacting domain; SID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori selected interacting domain (SID) protein #496.
                                                                                                                                                                                                                                                                                                                                                                 293 YLHTHPNAYLDMLYENPLATLDGKAYFYQDLSFKXILDFFKTILENDTIYH 343
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                                                                                                                                                                                                                                                             11.6%; Score 51; DB 9; L
100.0%; Pred. No. 9.5e-42;
tive 0; Mismatches 0;
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Gaps

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Local Similarity

51;

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Labigne A;

De Reuse H,

Colland F,

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The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complexes of protein-protein interactions in Helicobacter pylori, ful for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein-protein interaction; ulcer; selected interacting domain; SID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 205; 642pp; English.
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                                                                                                                                    28-DEC-2001; 2001WO-EP015428
                                                                                                                                                                                                   02-JAN-2001; 2001US-0259302P
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Matches 46; Conservative
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WO200266501-A2
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                                                                                                                               The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which modulate the interaction of proteins used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue
                       New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complexes of protein-protein interactions in Helicobacter pylori, it for identifying modulating compounds for treating or preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Labigne A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 MLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPF
                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Score 44; DB 5; Le 100.0%; Pred. No. 2.3e-35;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 2.34
Matches 44; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 204; 642pp; English.
                                                                                                       Claim 6; Page 305; 642pp; English
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N-PSDB; ABX65895.
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N-PSDB; ABX66310
                                                                                                                                                                                                                                                                                                                                                       Sequence 89 AA;
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Labigne A;

De Reuse H,

Colland F,

10.5%; Score 46; DB 5; Length 124; 100.0%; Pred. No. 3.1e-37; ive 0; Mismatches 0; Indels

(first entry)

amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue 888888

Sequence 169 AA;

Gaps ö Query Match
10.0%; Score 44; DB 5; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 44; Conservative 0; Mismatches 0; Indels

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304 MIYENPINTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPF 347

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Search completed: August 11, 2006, 20:00:03 Job time : 117.721 secs

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OM protein - protein search, using sw model

August 11, 2006, 20:00:25 ; Search time 20.6557 Seconds Run on:

(without alignments) 2049.570 Million cell updates/sec

US-10-764-212-18 Title: Perfect score:

440 1 MFQPLLDAFIESASIKKOMPL......YHKSLPLLRAIRRWVKKLGL 440 Sequence:

Gapop 60.0 , Gapext 60.0 OLIGO Scoring table:

283416 segs, 96216763 residues Searched:

Н Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 80:\* Database :

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	fucosyltransferase	fucosyltransferase		alpha (1,3)-fucosy	ш	probable regulator	hypothetical prote	heat shock gene re	conserved hypothet	hypothetical 80K p	surface-layer 125K	copia polyprotein	ZK112.7 protein -	probable pyrophosp	probable nucleotid	hypothetical prote	hypothetical prote	Q.	hypothetical prote	g	l-i	shikimate kinase (	shikimate kinase (			hypothetical prote	a	C 3	8
	ID	C64601	C64567	G71862	B71914	T09482	A87080	872958	F81676	T37941	B33856	A33856	OFFFCP	S44887	AC0264	C97249	B90131	H97620	AG2843	T26882	B71464	H84992	AC1000	AD0019	G83712	C90170	E64443	AI0696	E84078	A65134
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	Match Length	476	425	436	454	667	287	354	392	959	745	1176	1409	3343	128	152	153	162	162	169	172	173	173	173	174	177	184	215	215	240
* Query	Match	12.5	11.6	9.5	9.5	2.0	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.6	1.6	1.6	1.6	1.6	1.6	1.6	•	•		•		•	1.6	1.6	1.6
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H91157 P86003 S39656	T22978 B87434 G96545	S50964 H71876 A64640	F86864 B75101 T41507	DESPGA AG3582 E84043 AC2601	
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30 32 32	3 4 3 3 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 37 38	39 41	4 4 4 4 54 50 4 50	

### **ALIGNMENTS**

_	- 51244
	C645011 1
_	fucosyltransferase - Helicobacter pylori (strain 26695)
	C, Species: Helicobacter pylori
	C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
_	C;Accession: C64601
	R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
	Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne)
	son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
	Nature 388, 539-547, 1997
	A; Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
	A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
	A;Reference number: A64520; MUID:97394467; PMID:9252185
	A;Accession: C64601
	A, Status: preliminary; nucleic acid sequence not shown; translation not shown
	A; Molecule type: DNA
_	A;Residues: 1-476 <tom></tom>
	A,Cross-references: UNIFROT:025366; UNIFARC:UP100000D70CB; GB:AE000578; GB:AE000511; NID:
	Query Match 12.5%; Score 55; DB 2; Length 476;
_	
	Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy 293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPF 347
	Dh 297 YI-HTIPDNAY,DMLYRRPLINTI,DCKAYPYODLEFKYLLDFFKYLLDFFYTLENDTYYHNDF 351
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RESULT 2

fucosyltransferase - Helicobacter pylori (strain 26695)

Cispecies: Heliochacter pylori Cispecies: Heliochacter pylori Cispecies: Heliochacter pylori Cispecies: Heliochacter pylori Cispecies: Heliochacter pylori Cispecies: Os-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004 Ciscession: C64567 Cispecies: Walte, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, S.; Loftus, B.; Kalley, J.W.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A;Reference number: A64520; MUID:97394467; PMID:9252185 A;Reference number: A64520; MUID:97394467; PMID:9252185 A;Reterence number: A64520; Mullipary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-425 <TOM> A;Cross-references: UNIPROT:O25142; UNIPARC:UP100000070CA; GB:AE000554; GB:AE000511; NID:

Gaps ö Query Match
11.6%; Score 51; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 51; Conservative 0; Mismatches 0; Indels

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293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYH 343

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-667 <PER>
A;Crossidues: UNIPROT:015344; UNIPARC:UP1000012F0B6; EMBL:AF035360; NID:g2827993; I
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A;Rosidues: 1.334 «SMI>
A;Cross-references: UNDPROT:Q49889; UNIPARC:UPI0000B09BA; EMBL:U00021; NID:g467141; PIDN
C;Superfamily: regulatory protein spood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2011, 2011, 2011, A;Authores: Rutter, S.; Seeger, K.; Simon, S.; Simonds, M.; Skelton, J.; Squares, R.; SqnArtle: Massive gene decay in the leprosy bacillus.
A;Reference number: A66909; MUID:21128732; PMID:11234002
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C;Date: 19-Mar.1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 19-Mar.1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 872258
R;Smith, D.R.; Robison, K.
R;Smith, D.R.; Robison, K.
R;Buth, D.R.; Robison, M.
A;Description: Mycobacterium leprae cosmid L247.
A;Reference number: S72589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Mycobacterium leprae
C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C.Accession: A87080
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                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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100.0%; Pred. No. 7.6;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 1.2
Matches 9; Conservative 0; Mismatches
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C,Superfamily: rfp transforming protein
F;6-65/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: regulatory protein spo0J
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Matches 8; Conservative
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A;Status: preliminary
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C'Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C'Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C'Accession BJ1914
R'Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Alature 397, 176-180, 1999
Nature 397, 176-180, 1999
A'Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-436 cARNA
A;Gress-references: UNIPROT:Q9ZKD7; UNIPARC:UPI00000D36D2; GB:AE001528; GB:AE001439; NID
A;Experimental source: strain J99
                                                                                                                                                                                                                                          C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71862
C;Accession: G71862
I.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
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A;Experimental source: strain J99
C;Genetics:
A;Gene: fuct
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10948
R;Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A;Description: The human FXY maps to chromosome Xp22.3: Implications for evolution of A;Reference number: 216687
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                297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIXH 347
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                                                                                                                                                                                                                      alpha-(1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 DFKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQ 324
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Matches 42; Conserva
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Best Local Similarity
Matches 42; Conserva
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A,Status: preliminary
A,Molecule type: DNA
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R;Bowditch, R.D.; Baumann, P.; Yousten, A.A.
J. Bacteriol. 171, 4178-4188, 1989
A;Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer prote
A;Reference number: A33856; MUID:89327128; PMID:2666389
A;Accession: A33856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia
N;Contains: copia protein, 31K; copia protein, 48K; proteinase
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A03324; S03612; $\overline{814835}$
R;Mount, S.M.; Rubin, G.M.
Mol. Cell. Biol. 5, 1630-1638, 1985
A;Fitle: Complete nucleotide sequence of the Drosophila transposable element copia: homol A;Reference number: A03324; MUID:85267679; PMID:2410772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P38537; UNIPARC:UP10000135A02; GB:M28361; NID:g341911; PIDN:7 P;93-147/Domain: S-layer repeat homology <SLR2>
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A; Residues: 1-1409 <MOU>
A; Residues: 1-1409 <MOU>
A; Residues: 1-1409 <MOU>
A; Cross-references: UNIPROT: P04146; UNIPARC: UP10000127EE3; GB: M11240; NID: g158615; PIDN: P;
B; Miller, K.; Rosenbaum, U; Zbrzezna, V.; Pogo, A.O.
B; Miller, The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A; Title: The nucleotide sequence of Prosophila melanogaster copia-specific 2.1-kb mRNA.
A; Reference number: S03612; MUID: 89183629; PMID: 2538806
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A,Residues: 1-391,1375-1409 <MIL>
A,Residues: 1-391,1375-1409 <MIL>
A,Residues: 1-391,1375-1409 <MIL>
A,Cross-references: UNIPARC:UPI000002A70E; EMBL:X13719; NID:g7745; PIDN:CAA31997.19 PID:gR;Yoshioka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba, T.
EMBO J. 9, 535-541, 1990
A,Title: Virus-like particle formation of Drosophila copia through autocatalytic processi
A,Reference number: S14835; MUID:90151630; PMID:1689241
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A;Cross-references: UNIPARC:UPI000002A70E; EMBL:X54147; NID:97749; PIDN:CAA38086.1; PID:
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C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33856
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                                                                                                                              DB 2;
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100.0%; Pred. No. 23;
Live 0; Mismatches
                                                                                                                       Query Match
1.8%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches
A;Molecule type: DNA
A;Residues: 1-745 <BOW>
A;Cross-references: UNIPARC:UPI000017ACA5
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                                                                                                                                                                                                                                                                                                                     16 TLDGKAYF 23
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A;Molecule type: DNA
A;Residues: 1-1176 <BOW>
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C.Species: Bacillus sphaericus
C.Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993
C.Accession: B33856
J. Bacteriol. 171, 4178-4188, 1989
A;Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer prot
A;Accession: B33856, MUID:89327128; PMID:2666389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 «IEET»
A;Cross-references: UNIPROT:PS4306; UNIPARC:UPI00000579FA; GB:AE002336; GB:AE002160; NIC
                                                                                                                                                                                                                                                                                 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Mucleic Acids Ree. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mesidues: 1-656 <MCD>
A;Cross-references: UNIPROT:Q9UUJ6; UNIPARC:UPI000012FEF3; EMBL:AL109820; PIDN:CAB52577.
A;Experimental source: strain 972h-; cosmid c1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein SPAC1952.13 - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Dates: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Accession: 137941 R; McJougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T. submitted to the EMBL Data Library, August 1999 A; Reference number: 221755
                                                                                                                                                         heat shock gene repressor HcrA TC0673 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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100.0%; Pred. No. 8.3;
:ive 0; Mismatches
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 LVSIDDLR 160
164 EPLVSIDD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 LVSIDDLR 364
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Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: SPDB: SPAC1952.13
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Matches 8; Conserv
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                                                                                                                                                                                                                                                             C;Accession: F81676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
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Search completed: August 11, 2006, 20:09:15 Job time : 22.6557 secs
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A;Molecule type: DNA
A;Residues: 1-152 <KUR>
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C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession A.C0264
R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nytute 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-3343 <DUZ>
A;Cross-references: UNIPROT:P34616; UNIPARC:UP1000013BC7C; EMBL:L14324; NID:9289740; PIE
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZKI12.7 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S44887
R;Du, Z.
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1.8%; Score 8; DB 2; Length 3343;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Query Match
1.8%; Score 8; DB 1; Length 1409;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels
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A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyprotein
C;Keywords: polyprotein; proteinase
F;2-433/Product: copia protein, 48K #status predicted <WAT1>
F;2-270/Product: copia protein, 31K #status predicted <WAT2>
F;2-11-433/Product: proteinase #status predicted <WAT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid ZK112.
A;Reference number: S44616
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100.0%; Pred. No. 32;
tive 0; Mismatches
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Matches 7; Conservative
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A/Molecule type: DNA
A/Residues: 1-128 <KUR>
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A;Status: preliminary
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probable nucleotide-binding protein, YjeE family [imported] - Clostridium acetobutylicum (species: Clostridium acetobutylicum (species: Clostridium acetobutylicum (species: Clostridium acetobutylicum (species: Clostridium acetobutylicum (species: Clostridium acetobutylicum (species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004 (species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004 (species: 14-Sep-2001 #sequence_revision 183, 4823-4838, 2001

A;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Spacesion: C97249

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Residues: preliminary
A;Residues: 1-152 «KOR»
A;Residues: USOPFA2; UNIPARC:UPI0000CA65A; GB:AE001437; PIDN:AAK80782.1;
A;Residues: Local similarity 100.0%; Pred. No. 38;
Best Local Similarity 100.0%; Pred. No. 38;
Best Local Similarity 100.0%; Pred. No. 38;
Best Local Similarity 100.0%; Pred. No. 38;
Best Local Similarity 100.0%; Pred. No. 38;
Best Local Similarity 200 (specimal parameters)

A) Algebre 103 YAIGFDE 109

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Q9CC29_MYCLE
Q2S6L7_9SPHI
Q8FU16_COREF
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Gapop 60.0 , Gapext 60.0
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2: uniprot_trembl:*
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OBNZF1_STRPB RUVB_HELHP QZNIZG_SWOLU GJBZCS_BACTI GJ8BS9 WYCLE GBKSW1_STRP1 GJ8KW1_STRP1 GJ7VPA1_HELHP GJ8RR1_STRP1 GJ8WN7_STRP1 GJ8WN7	ALIGNMER  ALIGNMER  I. (EC 2.4.  (EC 2.4.  (EC 2.4.  (EC 2.4.  (EC 2.4.  (EC 2.4.  (A)  (A)  (A)  (A)  (A)  (A)  (A)  (A	Score 58; DB 2; I Pred. No. 6.3e-51; ; Mismatches 0; VTEXIIDAYFSHTIPIYWG	
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3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	11. 1 31 HELPY 032631, 01-32831, HELPY PRELIM 032631, 01-JAN-1998, integrat. 01-JAN-1998, sequence 07-FEB-2006, entry ver Alpha-(1,3)-fucosyltr: Name=fucT; Name=fucT	Query Match Best Local Simil Matches 58; C	106 2 HBLPY 25366_HB
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GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0004757; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
GO; GO:0016486; P:protein amino acid glycosylation; IEA.
Interbro; IPR001503; Glyco_trans_10.
Interbro; IPR001503; Glyco_trans_10; 1.
Complete proteome; Glycosyltransferase.
ECOMPLETE: A16 AA; 55927 MM; 32BFPDBBD36E1F74 CRC64;
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;
Ge Z., Chan N.W.C., Palcic M.M., Taylor D.E.,
"Cloning and heterologous expression of an alphal, 3-fucosyltransferase gene from the gaetric pathogen Helicobacter pylori.";
J. Biol. Chem. 272:21357-21363(1997).
                                                                                                      [1]

WUCLEDTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.K.,

Blougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,

Peterson S.M., Loftus B.J., Richardson D.L., Dodson R.J., Kalak H.G.,

Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,

Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,

Kelley J.M., Cotton M.D., Weidman J.F., Flylid C., Bowman C.,

Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,

Smith H.O., Fraser C.M., Venter J.C.;
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GO; GO:0016020; C:membrane; IEA.
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PIR; C64601, C64601.
TIGR; HP0551; -
LinkHub; 025366; -.
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Best Local Similarity
Matches 55; Conserv
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                                                                                   NCBI_TaxID=210;
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GO; GO: 0016620; C:membrane; IEA.
GO; GO: 00101675; F:tucosyltransferase activity; IEA.
GO; GO: 00101757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO: 0006486; P:protein amino acid glycosylation; IEA.
Interpro; IPR001503; Glyco_trans_10.
Interpro; IPR01503; Glyco_trans_10.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 425 AA; 49329 MW; I182AF180D124A34 CRC64;
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0006486; F:protein amino acid glycosylation; IEA.
InterPro; IPRO1503; Glyco_trans 10.
PANTHER; PTRR11929; Glyco_trans 10; 1.
Glycosyltransferase; Transferase.
SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=26695 / ATCC 700392;

MEDLINE=9739467; PubMed=9252185; DOI=10.1038/41483;

MEDLINE=9739467; PubMed=9252185; DOI=10.1038/41483;

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Kelley J.M., Cotton M.D., Weidman J.F., Frijii C., Bowman C.,

Watthey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D.,

Smith H.O., Fraser C.M., Venter J.C.,

"The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                 239 QGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 QGYGYYTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDY 293
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                                                                                                                                                                                                                                                                                         Length 478;
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OrderedLocusNames=HP0379; ORFNames=HP_0379;
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PIR; C64567; C64567.
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07-FEB-2006, entry version 24.
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Matches 52; Conservative
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Best Local Similarity
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glycosyl. . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA (1,3)-FUCOSYLTRANSFERASB.
Name-fucT; ORFNames=1hp_0596;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOCYC: HPYL85963:JHP0596-MONOMER; -.

BIOCYC: HPYL85963:JHP0596-MONOMER; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:tucosyltransferase activity; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

GO; GO:0016486; P:protein amino acid glycosylation; IEA.

InterPro; IRR001503; Glyco trans 10.

PANTHER; PTHR11929; Glyco-trans 10.

COMplete proteome; Glycosyltransferase; Transferase.

SEQUENCE 454 AA; 53448 MM; 3262687131263AB0 CRC64;
                                                                                                                                                                                                      Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring gl;
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
                                                                                                                                                                                                                                                                                                                                       283 DFKNFDEAIDYVRYLHTHPNAYLDMLYENPINTLDGKAYFYQ 324
                                                                                                                                                                                                                                                                                                        280 DFKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQ 321
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                                                                     InterPro; IPR001503; Glyco trans 10.
PANTHER; PTHR11929; Glyco trans 10; 1.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 436 AA; 50699 MM; 1DB2066AE98PA61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 DFKNFDEAIDYVRYLHTHPNAYLDMLYENPLNTLDGKAYFYQ
                                                                                                                                                                                                   9.5%; Score 42; DB 2; Le
100.0%; Pred. No. 3.6e-34;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 42; DB 2; Li
100.0%; Pred. No. 3.7e-34;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacteraceae; Helicobacter
NCBI_TaxID=85963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZLI3 HELPJ PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                         42; Conservative
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                                                                                                                                                                                                                             Best Local Similarity
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Q9L8S4;
01-OCT-2000, i
01-JUN-2003, 8
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:tucosyltransferase activity; IEA.
GO; GO:00160757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
Glycosyltransferase; Transferase.
Glycosyltransferase; Transferase.
SEQUENCE 432 AA; 50503 MW; 69D3A32FBD2F12C9 CRC64;
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=99120557; PubMed=9921682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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"Molecular Cloning and Functional Expression of a Novel Helicobacter
pylori (alpha)-1,4 Fucosyltransferase.";
Glycobiology 15:1076-10831(2005).
                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MX-1999, integrated into UniProtKB/TrEMBL.
01-MX-1999, sequence version 1.
21-FBB-2006, entry version 23.
ALPHA-(1,3)-FUCOSYLTRANSFERASE.
Name=fucU; ORFNames=jhp_1002;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 ESDPLKRGFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 BSDPLKRGFASFVASNPNAPKRNAFYDALNSIEPVTGGGSVKNTLGY 217
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2.2e-39;
                                                   05-JUL-2004, integrated into UniprotKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
       432 AA.
                                                                                                                                                                                                                                                                                                                                 STRAIN=DSM 6709;
PubMed=16000696; DOI=10.1093/glycob/cwj004;
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100.0%; Pred. No. 2.27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZKD7 HELPJ PRELIMINARY; PRT;
Q9ZKD7;
       Q6ST35 HELPY PRELIMINARY; PRT;
                                                                                                                                                                                                                          Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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GO; GO:0016020; C:membrane; IEA.
                                                                                                                                Alpha-1,4 fucosyltransferase.
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Best Local Similarity
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RESULT 6

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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mastomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
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94 94
94 AA; 10617 MW; 1485630849C1B84F CRC64;
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                                                                               Score 9; DB 2;
Pred. No. 2;
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                                                                               2.0%; Score 9; DB 2
100.0%; Pred. No. 2;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus cervicolor (Fawn-colored mouse)
                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001870; B302.
InterPro; IPR001879; Butyrophylin.
InterPro; IPR003877; SPRY_rcpt.
Pfam; PF00622; SPRY; I
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003, integrated into Uni
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 12.
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NON TER 1 1 1
NON TER 94 94
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                          9; Conservative
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Name=Fxy;
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Best Local Similarity
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Mastomys huberti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10097;
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Q80Z78;
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QB0Z75 MUSCE
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006410; F:fucosyltransferase activity; IEA.
GO; GO:0006486; F:fucosyltransferase activity, transferring glycosyl. . .; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
FANTHER; PTHR11929; Glyco_trans 10.
FANTHER; PTHR11929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 462 AA; 54560 MW; BD27F8B35IECE752 CRC64;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=XBS;
MEDLINE=22503854; Pubmed=12615004; DOI=10,1016/S0168-9525(03)00021-0;
                                                                                                                                                                                                         Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
"Cloning and characterization of the alpha(1,3/4) fucosyltransferase of Helicobacter pylori.";
Biol. Chem. 275:4988-4994(2000).
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                                          Helicobacter pylori (Campylobacter pylori).
Bacteria; Froteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
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                                                                                                                                                                                        MEDLINE=20138242; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                          Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 7.3%; Score 32; DB 2; Lu
Local Similarity 100.0%; Pred. No. 9.6e-24;
es 32; Conservative 0; Mismatches 0;
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InterPro; IPR001897; B302.
InterPro; IPR003879; Butyrophylin.
InterPro; IPR003877; SPRY_ropt.
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      Alpha-1,3/4-fucosyltransferase
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STRAIN=UA948;
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                                                                                                                                                                                                                                                                                                                                     STRAIN=UA948;
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Best Loca Matches

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NCBI_TaxID=10103;
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Q810Y0;
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE.
MEDIJNE=22503854; Pubmed=12615004; DOI=10.1016/S0168-9525(03)00021-0; MEDIJNE=22503854; Pubmed=12615004; DOI=10.1016/S0168-9525(03)00021-0; Montoya-Burgos J.I., Boursot P., Galtier N.; Recombination explains isochores in mammalian genomes."; Trends Genet. 19:128-130(2003).
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  #EDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
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                        Montoya-Burgos J.I., Boursot P., Galtier N.; "Recombination explains isochores in mammalian genomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                           94 AA; 10617 MW; 1485630849C1B84F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.0%; Score 9; DB 2;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches
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100.0%; Pred. No. 2;
tive 0; Mismatches
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InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophylin.
InterPro; IPR003877; SPK_rcpt.
Pfam; PF00622; SPKY; 1.
PRINTS; PR01407; BUTYPHINCDUF.
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InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophylin.
InterPro; IPR003877; SPRY_ropt.
Pfam; PF00622; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arvicola terrestris (European water vole)
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Q80ZBS MUSPL
ID Q80ZBS_MUSPL PRELIMINARY;
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es 9; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                            Fxy (Fragment).
Mus platythrix (Plat-haired mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22503854; PubMed=12615004; DOI=10.1016/S0168-9525(03)00021-0;
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01-JUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 11.
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InterPro; IPR001870; B302.
InterPro; IPR001879; Butyrophylin.
InterPro; IPR003877; SPRY_ropt.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHINCDUF.
NON_TER 94 94
SEQUENCE 94 AA; 10587 MW; 123565BEF9C7084
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100.0%; Pred. No. 2;
tive 0; Mismatches
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InterPro; IPR001870; B302.
InterPro; IPR003879; Butyrophylin.
InterPro; IPR003877; SPRY_rcpt.
Pfam; PF00622; SPRY; 1.
PRINTS; PR01407; BUTYPHINCDUF.
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                                                                                                                                                                                                     Muroidea; Muridae; Murinae; Mus NCBI_TaxID=10101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2002, integrated into UniProtKB/Swiss-Prot.
01-UNA-2000, sequence version 1.
07-MAR-2006, entry version 3.
Midline-1 (Tripartite motif protein 18) (Fragment).
Name=Midl; Synonyms=Fxy, Trim18;
Mus caroli (Wild mouse) (Ricefield mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=99439873; PubMed=10508587; DOI=10.1016/S0960-9822(99)80430-8;
Perry J., Ashworth A.;
"Evolutionary rate of a gene affected by chromosomal position.";
Curr. Biol. 9:987-989(1999).
-!- FUNCTION: May have E3 ubiquitin ligase activity which targets the catalytic subunit of protein phosphatase 2 for degradation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SUBUNIT: Homodimer or heterodimer with MID2. Interacts with IGBP1
(By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; microtubule-associated (By
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                         DB 2; Length 94;
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94 AA; 10617 MW; 1485630849C1B84F CRC64;
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PRINTS; PR01407; BUTYPHINCDUF.
Ligase; Metal-binding; Microtubule; Phosphorylation; Ull conjugation pathway.
CHAIN 1108
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-!- SIMILARITY: Belongs to the TRIM/RBCC family.
-!- SIMILARITY: Contains 1 B30.2-like domain.
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MGI; MGI:1100537; Midl:
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Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches
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InterPro; IPR003879; Butyrophylin.
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InterPro; IPR001841; Znf_RING.
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Search completed: August 11, 2006, 20:08:08 Job time : 159.082 secs

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RESULT 1
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Sequence 3, Application US/09092315
Patent No. 639937
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 1998-06-05
BARLIER APPLICATION NUMBER: US 60/048,857
EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Matches 440; Conservative
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US-10-392-098A-3
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LENGTH: 440
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION WUMBER: US/09/733,524A
FRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
NHOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
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DDLRADYNNLRADYNNLRADYNNLRADYNNLRADYDRLLGNRSPLLBLSQNTTFKIYHKA 420
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 440; Conservative 0; Mismatches 0;
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; Sequence 3, Application US/09733524A
; Patent No. 6534298
; GENERAL INFORMATION:
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                                                                 421 YHKSLPLLRAIRRWVKKLGL 440
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US-09-733-524A-3
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LENGTH: 440
TYPE: PRT
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RESULT 3 ES-10-189-977A-3

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Sequence 3, Application US/10189977A
Patent No. 6962806
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION NUMBER: US/09/733,524
PRIOR PELICATION NUMBER: US 09/092,315
PRIOR PELICATION NUMBER: US 60/048,857
PRIOR PELICATION NUMBER: US 60/048,857
PRIOR PELICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FREEXEQ for Windows Version 4.0
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Patent No. 7029891
GENERAL INFORMATION SIGNATION APPLICANT: Taylor, Diane E. APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/392,098A
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US-10-189-977A-3
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                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: H. pylori strain UA802
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpPucT)
US-10-392-098A-3
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongmaing
ITILE OF INVENTION: ALFEA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT PILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 2000-12-07
SOFTWARE: PACENTIN NUMBER: US 09/733,524
SOFTWARE: PACENTIN VET: 2.1
SEQ 1D NO 3
LENGTH: 440
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ORGANISM: Helicobacter pylori
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GENERAL INCORMATION:

APPLICANT: Taylor, Diane R.

APPLICANT: Taylor, Diane R.

APPLICANT: Taylor, Diane R.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: PUCCSYLIRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US 09/092,315

PRIOR PILING DATE: 2000-12-07

PRIOR PLILING DATE: 1999-06-05

PRIOR PILING DATE: 1999-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PASCSEQ for Windows Version 4.0
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: G. Zhongming
TITLE OF INVENTION: RUCGSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-04902
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/10/189, 977A
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-06
PRIOR FILING DATE: 1998-06-06
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                                                                                                                                                                                         0; Gaps
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Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                    Query Match
13.2%; Score 58; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 58; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 454
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; Sequence 8, Application US/10189977A
; Patent No. 6962806
                              ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-092-315-8
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ORGANISM: Helicobacter pylori
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ORGANISM: Helicobacter pylori
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LENGTH: 454
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Best Local Similarity 100.0%; Pred. No. 1.4e-45; Matches 55; Conservative 0; Mismatches 0;
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                                                 Query Match 13.2%; Score 58; DB 2; Length 454; Best Local Similarity 100.0%; Pred. No. 1.5e-48; Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.2%; Score 58; DB 3; Length 454; Best Local Similarity 100.0%; Pred. No. 1.5e-48; Matches 58; Conservative 0; Mismatches 0; Indels
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
ITILE OF INVENTION: ALFA-1, 3-FUCOSYLTRANFERASE;
FILE REFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT PILING DATE: 1990-06-05
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                GENERAL INCRMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/120,319
PRIOR APPLICATION NUMBER: US/10/120,319
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PLING DATE: 1997-06-06
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1908-06-05
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE PARCHIN Ver. 2.1
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Patent No. 7029891
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Patent No. 6399337
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ORGANISM: Helicobacter pylori
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US-10-392-098A-8
  US-10-189-977A-8
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Sequence 5, Application US/09733524A

Sequence 5, Application US/09733524A

Patent No. 6534298

GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: PUCCSYLTRANSFRASES AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: BXPRESSING THEM (amended)

TITLE OF INVENTION: BXPRESSING THEM (amended)

TITLE OF INVENTION: BXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US 09/092,315

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FRESSEQ for Windows Version 4.0
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION NUMBER: US/09/733,524
PRIOR PILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE PRESEQ for Windows Version 4.0
SSO ID NO 5
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Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels
Indels
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; ORGANISM: Helicobacter pylori
US-10-189-977A-5
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293 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPF 347
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                               297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFYKILDPFKTLLENDTIYHNNPF 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: H. pylori strain 26695A
; OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-098A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%; Score 55; DB 3; Length 476; 100.0%; Pred. No. 1.4e-45; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                    GENERAL NO. //28931;
GENERAL NO. //28931;
APPLICANT: Taylor, Diane E. APPLICANT: Taylor, Diane E. APPLICANT: Ge, Zhongming is APPLICANT: University of Alberta APPLICANT: University of Alberta TILLE OF INVENTION: Alpha-1,3 Fucosyltransferase; TILLE REFERENCE: 017398-000420US; CURRENT APPLICATION NUMBER: US/10/392,098A; CURRENT APPLICATION NUMBER: US/10/120,319; PRIOR PILING DATE: 2002-04-09; PRIOR PILING DATE: 1999-06-06; PRIOR FILING DATE: 1999-06-05; PRIOR PILING DATE: 1998-06-05; PRIOR PILING DATE: 1998-06-05; PRIOR PILING DATE: 1998-06-05; PRIOR PILING DATE: 2000-12-07; NUMBER OF SEQ ID NOS: 30
SOFTWARE PARENTIN Ver. 2.1
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Patent No. 6399337
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: US/09/092,315
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SEQTWARE: PASESEQ for Windows Version 3.0
SEQTUAND 13
                                                                                                               RESULT 12
US-10-392-098A-5
; Sequence 5, Application US/10392098A
; Sequence 100, 7029891
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ORGANISM: Helicobacter pylori
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ORGANISM: Helicobacter pylori
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Best Local Similarity 100.0
Matches 55; Conservative
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Sequence 1, Application US/09733524A

Patent No. 6534298
GENERAL INPORMATION:
TRIAL INPORMATION:
TITLE OF INVENTION: WICKLETC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
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TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1997-06-06
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                           Sequence 1, Application US/09092315
Patent No. 639937
GENERAL INFORMATION:
APPLICANT: TAYLOR, Diame B.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE;
FILE REFERENCE: 07254/049001
CURRENT FILLING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: US/09/092,315
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER APPLICATION NUMBER: US 60/048,857
HAUNBER OF SEQ ID NOS: 22
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11.8%; Score 52; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 52; Conservative 0; Mismatches 0;
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US-09-092-315-1
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ORGANISM: Helicobacter pylori
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US-09-092-315-1
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2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

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US-10-120-319-8
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    protein search, using sw model

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; Sequence 3, Application US/10120319
; Publication No. US2020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OP INVENTION: ALPHA-1,
; FILE REFERENCE: 07254/04901,
; CURRENT FILING DATE: 2002-04-09
; CURRENT PILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
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US-10-764-212-68
US-09-733-524-2
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US-11-189-977-2
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US-10-189-977-2
US-10-189-977-2
US-10-189-977-2
US-10-184-68-5
US-10-184-68-23
US-10-764-212-6
US-10-764-212-6
US-10-764-212-7
US-10-764-212-7
US-10-764-212-7
US-10-764-212-7
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100.0%; Pred. No. 0;
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TYPE: PRT
ORGANISM: Helicobacter pylori
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Best Local Similarity 100.
Matches 440; Conservative
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PUblication No. US20030166211A1
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT PILING DATE: 2002-07-03
PRIOR PULICATION NUMBER: US/09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARR: FASTSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 440; Conservative 0; Mismatches
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ORGANISM: Helicobacter pylori
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LENGTH: 440
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RESULT 3 US-10-392-098-3 2. Sequence 3, Application US/10392098

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GENERAL INFORMATION:

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: PUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/0/392,098

CURRENT APPLICATION NUMBER: US/09/733,524A

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 440

TYPE: PRI
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Publication No. US20050164338A1
GENERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Roses Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
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US-10-392-098-3
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Matches 440; Conservative
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ORGANISM: Helicobacter Pylori fucosyltransferase
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Fatent No. US20020068347A1
GENERAL INFORMATION:
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM
TITLE OF INVENTION: EXPRESSING THEM
TITLE OF INVENTION: EXPRESSING THEM
TITLE OF INVENTION: UNMBER: US/09/733,524
CURRENT PILING DATE: 2000-12-14
PRIOR PPLICATION NUMBER: 09/092,315
PRIOR PPLICATION WUMBER: 60/048,857
PRIOR PLING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 20
SOFTWARR: FASTSEQ FOR Windows Version 4.0
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                                                                                                                                            FEATURE:
; OTHER INFORMATION: H. pylori strain 802 FutA fucosyltransferase
US-10-764-212-18
                                                                                                                                                                                                            100.0%; Score 440; DB 5; Length 440; 100.0%; Pred. No. 0; cive 0; Mismatches 0; Indels
               CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 18
LENGTH: 440
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 FILE REFERENCE: 019957-019400US
                                                                                                               TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 440; Conservative
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LENGTH: 440
TYPE: PRT
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APPLICANT: TASCORNATION:
APPLICANT: TAYLOR:
APPLICANT: TAYLOR:
APPLICANT: TAYLOR:
APPLICANT: TAYLOR:
APPLICANT: TAYLOR:
APPLICANT: G. Zhongming
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCOSYLTRANSFERASE, AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: FUCOSYLTRANSFERASE, AND EXPRESSION SYSTEMS FOR MAKING AND
FILLS REFERENCE: 07254/049002
CURRENT PILLOR DATE: 2000-12-14
PRIOR PILLING DATE: 1998-06-05
PRIOR FILLING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE FREE FREESC for Windows Version 4.0
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                                                                                                                                                                                                                                                                             1 MFQPLLDAFIESASIKKMPLSYPPLKIAVANWWGGAEFKKKSAMYFILSQRYTITLHONP
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                Score 238; DB 3; Length 440;
Pred. No. 8.5e-220;
0; Mismatches 2; Indels
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ORGANISM: helicobacter pylori fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
COTION: Strain 11637 from NCTC11637
US-09-733-524-18
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
COTHER INPORMATION: Strain 802 from UA802
US-09-733-524-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHKSLPLLRAIRRWVKKLGL 440
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                                                                                                                                                                Query Match
Best Local Similarity 99.5%;
Matches 438; Conservative (
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                                                                                                                                                                                              227 EFLSQYKFULCFENSQGYGYVTEKIIDAYFSHTIPIIYMGSPSVAKDFNPKSFVNVHDF 284
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Fublication No. US20020164749A1
Fublication No. US20020164749A1
Fublication No. US20020164749A1
Fublication No. US20020164749A1
Fublication No. US20020164749A1
Fublication No. US20020164749A1
FILER REFERENCE: 07254/049001
FULSERT APPLICATION NUMBER: US/10/120,319
CURRENT PILING DATE: 2002-04-09
FRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
FRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
FRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE FREUES FILING DATE: 1997-06-06
FRIOR FILING DATE: FALLIER FILING DATE: 1997-06-06
FRIOR FILING DATE: FALLIER FILING DATE: 1997-06-06
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Length 454;
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APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-PUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
FRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NOS: 24
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   ch 13.2%; Score 58; DB 3; Lo
1 Similarity 100.0%; Pred. No. 9.9e-47;
58; Conservative 0; Mismatches 0;
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Publication No. US20030166211A1
GENERAL INFORMATION:
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; ORGANISM: Helicobacter pylori
US-10-189-977-8
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ORGANISM: Helicobacter pylori
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58; Conservative
Query Match
Best Local Similarity
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US-10-120-319-8
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227 EFLSÖYKFNLCFENSGGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 284

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Sequence 15, Application US/09733524

Sequence 15, Application US/09733524

Patent No. US20020068347A1

GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: PUCCSTLIRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: WOUGHIER 1050/733,524

TITLE OF INVENTION: EXPRESSING THEM

FILE REFERENCE: 07254/04902

CURRENT FILING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR PLING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 476
                                                                             APPLICANT: Taylor, biane E.
APPLICANT: Taylor, biane E.
APPLICANT: Taylor, biane E.
APPLICANT: Taylor, biane E.
APPLICANT: Taylor, biane E.
TITLE OF INVENTION: WICKLER AND EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: EXPRESSION THEM (amended)
FILE REPERRENCE: 07254-04902
FILE REPERRENCE: 07254-04902
CURRENT APPLICATION NUMBER: US/09/733,524A
PRIOR APPLICATION NUMBER: US/09/733,524A
PRIOR PLILING DATE: 2000-12-07
PRIOR PLILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PLILING DATE: 1997-06-06
NUMBER OF SEC ID NOS: 27
SOFTWARE: FastSEC for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.2%; Score 58; DB 4; I Best Local Similarity 100.0%; Pred. No. 9.9e-47; Matches 58; Conservative 0; Mismatches 0;
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ORGANISM: Helicobacter pylori fucosyltransferase
Sequence 8, Application US/10392098
Publication No. US20030166212A1
GENERAL INFORMATION:
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OTHER INFORMATION: Strain 26695A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ; ORGANISM: Helicobacter pylori
US-10-392-098-8
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Matches 55; Conservative
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NAME/KEY: PEPTIDE
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TYPE: PRT
ORGANISM: Helicobacter pylori
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  Zhongming
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Matches 52; Conserva
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US-10-189-977-13
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                                                                                                                                                                                                                                                                                                                                                   LENGTH: 476
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                                                                                                                                                  APPLICANT: TAYLOR. Jane B.
APPLICANT: TAYLOR. Diane B.
APPLICANT: TAYLOR. ALPHA-1, 3-FUCOSYLTRANFERASE
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT PILING DATE: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR PELICATION NUMBER: BARLIER APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FASTSEQ for Windows Version 3.0
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297 YLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNPF 351
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Publication No. US20030166211A1
GENERAL INFORMATION.
APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 2002-07-03
PRIOR PHLICATION NUMBER: US/10/189,977
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILOR DATE: 1998-06-06
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
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1 Similarity 100.0%; Pred. No. 7.9e-44;
55; Conservative 0; Mismatches 0;
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Publication No. US20020164749A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
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; ORGANISM: Helicobacter pylori
US-10-189-977-5
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Best Local Similarity
                                                            RESULT 11
US-10-120-319-5
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TITLE OF INVENTION: MUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
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APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07234/04901
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT FILING DATE: 2002-04-09
FRIOR PILING DATE: RARLIER APPLICATION NUMBER: 09/092,315
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: BARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.5%; Score 55; DB 4; Length 476; Best Local Similarity 100.0%; Pred. No. 7.9e-44; Matches 55; Conservative 0; Mismatches 0; Indels
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APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
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Pred. No. 4.9e-4
                                                                           CURRENT APPLICATION NUMBER: US/10/392,098
CURRENT APPLICATION NUMBER: US/10/392,098
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-06
NUMBER: OF SEQ ID NOS: 27
SEQ ID NO 5
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Publication No. US20020164749A1
GENERAL INFORMATION:
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100.0%; Pre
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Search completed: August 11, 2006, 20:16:19 Job time : 107.23 secs

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US-10-449-902-31893
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100767,
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/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
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/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-056-355B-67711
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US-11-056-355B-67710
US-11-056-355B-15997
US-11-056-355B-15996
US-11-056-355B-100768
US-11-056-355B-100768
US-11-056-355B-100766
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26 7 1.6 469 7 US-11-056-355B-8574 Sequence 8574, Ap 29 7 1.6 469 7 US-11-056-355B-17428 Sequence 17428, A 29 7 1.6 471 7 US-11-056-355B-8573 Sequence 17427, Ap 29 7 1.6 477 7 US-11-056-355B-17427 Sequence 17427, Ap 30 7 1.6 476 7 US-11-056-355B-8579 Sequence 17427, Ap 31 7 1.6 506 7 US-11-056-355B-8978 Sequence 3310, Ap 32 7 1.6 506 7 US-11-056-355B-8978 Sequence 3310, Ap 34 7 1.6 508 7 US-11-056-355B-8978 Sequence 31461, Ap 37 7 US-11-056-355B-8979 Sequence 17426, Ap 36 7 US-11-056-355B-89280 Sequence 17426, Ap 37 7 1.6 516 6 US-10-953-349-31461 Sequence 50279, Ap 37 7 1.6 516 6 US-10-953-349-31461 Sequence 50279, Ap 40 7 1.6 578 6 US-10-449-902-50578 Sequence 50279, Ap 41 7 1.6 578 6 US-10-449-902-50578 Sequence 50279, Ap 41 7 1.6 593 6 US-10-449-902-50578 Sequence 50279, Appli 4 7 1.6 615 6 US-10-519-335-6 Sequence 67279, Appli 4 7 1.6 625 6 US-10-519-335-6 Sequence 54865, Appli 4 7 1.6 628 6 US-10-519-335-4 Sequence 54865, Appli 5 Company 5 Company 5 Company 5 Company 5 Company 5 Company 5 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Company 6 Compan
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## ALIGNMENTS

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Sequence 15997, Application US/11056355B;
Sequence 15997, Application US/11056355B;
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE OF INVENTION: Polypeptides Encoded Thereby
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/544,190
SEQ ID NO 15997
LENGTH: 270
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Indels
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APPLICANT: BLOVET, VACHERIA

TITLE OF INVENTION: Sequence Determined DNA Fragment

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE REPERENCE: 2750-1590802

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR PILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 67711
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OTHER INFORMATION: Ceres Seq. ID no. 12407516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(259)
OTHER INFORMATION: Ceres Seq. ID no. 13595883
  Mismatches
                                                                                                                                                                                                                                Sequence 67711, Application US/11056355B; Publication No. US20060150283A1; GENERAL INFORMATION; APPLICANT: Brover, Vyacheslav
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ORGANISM: Zea mays subsp. mays
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ORGANISM: Triticum aestivum
7; Conservative
                                                      424 SLPLLRA 430
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LOCATION: (1)..(2)
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US-11-056-355B-67711
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     Matches
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Publication No. US20060107345A1
GENERAL INFORMATION:
FIGURE ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin Version 3.3
SOFTWARE: Patentin Version 3.3
SOFTWARE: Patentin Version 3.3
TYPE: REPRESENCE: 259
TYPE: REPRESENCE: 259
TYPE: PRT
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Publication No. US20060123505A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Poundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

TITLE REPRESENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: US/10/449,902

PRIOR APPLICATION NUMBER: US/202-203269

PRIOR APPLICATION NUMBER: JD 2002-203269

PRIOR APPLICATION NUMBER: JD 2002-16-10

PRIOR PRINT DE DESCRIPTION NUMBER: US/202-383870
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100.0%; Pred. No. 52;
vative 0; Mismatches 0; Indels
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1.6%; Score 7; DB 6
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches
  PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31893
LENGTH: 238
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 47233
LENGTH: 238
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Matches 7; Conservative
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US-10-449-902-47233
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US-10-449-902-31893
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Sequence 15996, Application US/11056355B

Publication No. US20060150283A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590FUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR FILING DATE: 2004-02-13

NUMBER: OF SEQ ID NOS: 119966

SEQ ID NO 15996
          APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Poundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/2002-203269
PRIOR PLING DATE: 2003-05-30
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
: SOFTWARE: Patentin Ver. 2.1
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APPLICANT: National Institute of Agrobiological Sciences.
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i_LCCATION: (301)...(301)

i_CTHER INFORMATION: Xaa is any aa, unknown or other

US-11-056-3558-15996
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LOCATION: (1)..(334)
OTHER INFORMATION: Ceres Seq. ID no. 12407515
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100.0%; Pred. No. 71;
tive 0; Mismatches
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; Publication No. U920060150283A1
; GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity 100.
Matches 7; Conservative
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CORGANISM: Oryza sativa
US-10-449-902-46731
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Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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; Sequence 67710, Application US/11056355B
; Sequence 67710, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 67710
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Pred. No. 60;
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100.0%; Pred. No. 60;
tive 0; Mismatches
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| LOCATION: (1)..(276)
| OTHER INFORMATION: Ceres Seq. ID no. 13595882
US-11-056-3558-67710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.6%; Score 7; DB (Best Local Similarity 100.0%; Pred. No. 60; Matches 7; Conservative 0; Mismatches
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Publication No. US20060123505A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%
Matches 7; Conservative
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; ORGANISM: Triticum aestivum
US-10-953-349-26635
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ORGANISM: Triticum aestivum
                         312 TLDGKAY 318
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LENGTH: 276
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312 TLDGKAY 318
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         CURRENT FILING DATE:
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NAME/KEY: peptide
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US-11-056-355B-112006
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Sequence 112007, Application US/11056355B

PUBLICATION NO. US20060150283A1

GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Wickolai
TILLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TILLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-44
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 112007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-11-056-355B-15995
Sequence 15995, Application US/11056355B
Sequence 15995, Application US/11056355B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brower, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590F025
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT APPLICATION NUMBER: US/11/056,355B
FRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 100768
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.6%; Score 7; DB 7; Best Local Similarity 100.0%; Pred. No. 72; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(339)
; OTHER INFORMATION: Ceres Seq. ID no. 13606035
US-11-056-355B-112007
                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: peptide
; LOCATION: (1)..(339)
; OTHER INFORMATION: Ceres Seq. ID no. 13606035
US-11-056-355B-100768
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CURRENT APPLICATION NUMBER: US/11/056,355B
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                          TYPE: prt
ORGANISM: Arabidopsis thaliana
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Les 7; Conservative
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                                                                                                                                                                                                                                                                                                                         FEATURE:
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APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 100767
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Publication No. US20060150283A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                NAME/KEY: misc feature; LOCATION: (324); OTHER INFORMATION: Xaa is any aa, unknown or other US-11-056-3558-15995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%; Score 7; DB 7;
100.0%; Pred. No. 76;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.6%; Score 7; DB 7;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 NUMBER OF SEQ ID NOS: 119966 SEQ ID NO 15995 LENGTH: 357
                                                                                                                        TYPE: prt
ORGANISM: Zea mays subsp. mays
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 100.
Matches 7; Conservative
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OTHER INFORMATION: Ceres
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0; Gaps
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## PRIOR APPLICATION NUMBER: 60/544,190
| PRIOR FILING DATE: 2004-02-13
| NUMBER OF SEQ ID NOS: 119966
| SEQ ID NO 112006
| LENGTH: 358
| TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | TYPE: prt | 
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346 TLDGKAY 352
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Search completed: August 11, 2006, 20:17:17 Job time : 17.7213 secs

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

August 11, 2006, 19:53:30 ; Search time 120.966 Seconds Run on:

(without alignments)
1723.552 Million cell updates/sec

US-10-764-212-20

456 1 MPQPLLDAPIDSTHLDBTTH......TSFKIYRKAYQKSLPLLRAI 456 Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

2589679 segs, 457216429 residues Searched: 2589342 Total number of hits satisfying chosen parameters:

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Listing first 45

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* Geneseq 8:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20068:\*

geneseqp2004s:\* geneseqp2005s:\*

SUMMARIES

## Result No.

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Description	Aeb70149 Helicobac	Aeb70154 H. pylori	Aeb70211 Helicobac	Abu52257 Helicobac		_	Adj27355 Alpha-1,3		Abg30884 H. pylori	He	Aeb70195 H. pylori	Adj77812 Helicobac	Adj27347 Alpha-1,3		Abg30887 H. pylori	_	Abu51151 Helicobac	Ξ.	Ξ.	He	Adj27349 Alpha-1,3		Adj77810 Helicobac	
, OI	AEB70149	AEB70154	AEB70211	ABU52257	ABG30885	ADJ77820	ADJ27355	AEB70141	ABG30884	AEB70145	AEB70195	ADJ77812	ADJ27347	AEB70133	ABG30887	ABG32639	ABU51151	AEB70190	ABG3 0882	ADJ77814	ADJ27349	AEB70135	ADJ77810	
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Length	456	22	559	418	42	42	42	425	47	446	39	432	432	432	45	4	169	17	48	48	485	485	48	
Query Match	100.0	44.1	44.1	14.9	14.9	14.9	14.9	14.9	14.9	11.0	10.1	10.1	10.1	10.1	9.0	8.6	8.6	8.6	8.6	8.6	8.6	8.6	8.6	
Score	456,	201	201	68	68	99	68	68	68	20	46	46	46	46	41	39	39	39	39	39	39	39	39	
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Adj27345 Alpha-1,3	Aeb70131 Helicobac	Aeb70212 Helicobac	Aeb70197 H. pylori	Aab10737 H. pylori	Abu51565 Helicobac	Aeb70147 Helicobac		Abg30886 H. pylori		Ħ	Ξ.	Ħ	Ξ	He	Adj27351 Alpha-1,3	Aeb70137 Helicobac	Abg30883 H. pylori		He		Adj77818 Helicobac
ADJ27345	AEB70131	AEB70212	AEB70197	AAB10737	ABU51565	AEB70147	AAW86008	ABG30886	ABU51720	AEB70202	AEB70201	AEB70205	AEB70199	ADJ77816	ADJ27351	AEB70137	ABG30883	ABG30881	ABU51590	AEB70193	ADJ77818
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8.6	8.6	8.6	7.9	7.7	7.0	7.0	7.0	7.0	6.4	6.4	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.9	5.5	5.0
39	39	39	36	35	32	32	32	32	53	53	28	28	28	28	28	28	28	28	27	22	23
24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 20. AEB70149 standard; protein; 456 AA (first entry) 06-OCT-2005 AEB70149; 

Fucosyltransferase; protein production; enzyme Helicobacter pylori; strain 948.

US2005164338-A1.

22-JAN-2004; 2004US-00764212. 28-JUL-2005.

(NEOS-) NEOSE TECHNOLOGIES INC. (UYAL-) UNIV ALBERTA.

22-JAN-2004; 2004US-00764212.

Johnson KF, Simala-Grant J, Taylor D, WPI; 2005-521417/53.

Bezila DJ;

New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids. N-PSDB; AEB70148

Claim 2; SEQ ID NO 20; 97pp; English.

The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosacchardes, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase prolyniciansferase polynucleotides and polypeptides are useful for the sequence is Helicobacter pylori fucosyltransferase protein.

Sequence 456 AA;

Query Match

Length 456; DB 9; 100.0%; Score 456; N

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                      SNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYL
                                                                                                                                                                                                                 GYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLHAHQN
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                                                       1 MFQPLLDAFIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILH
                                                                                                                          RMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGF
                                                                                                                                                                     ASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFENSQ
                                  1 MFQPLLDAFIDSTHLDETTHKPPLNVALANWWPLKNSEKKGFRDFILHFILKQRYKIILH
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             Gaps
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             Indels
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  ; Pred. No. 0; 0; Mismatches
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 100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Best Local Similarity 100. Matches 456; Conservative
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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of

Disclosure; SEQ ID NO 25; 97pp; English.

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fucose residue from a donor substrate to an acceptor substrate. The the discospitransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein fragment.
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                                                                                                                                                                                                                                                   PILKORYKI ILHSNPNEPSDLVFGNPLEQARKI LSYQNTKRVFYTGENEVPNFNLFDYAI
                                                                                                                                                                                                     GFDELDFNDRYLRMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCAL
                                                                                                                                                                                                                                       IHNESDPWKRGFASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLS
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                                                                                                                                       FILKORYKIILHSNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAI
                                                                                                                                                                                      GPDELDFNDRYLRMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCAL
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                                                                                      9; Length 227;
                                                                                                             Indels
                                                                                     44.1%; Score 201; DB 9; Le
100.0%; Pred. No. 3.8e-195;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fucosyltransferase; protein production; enzyme
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                                                                                                                                                                                                                                                                                                               QYKFNLCFENSQGYGYVTEKI 226
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                                                                                                                                                                                                                                                                                                                                                                             AEB70211 standard; protein; 559
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                                                                                   Query Match
Best Local Similarity 100.0
Matches 201; Conservative
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                                                               Sequence 227 AA;
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108

98 FILKQRYKIILHSNPNEPSDLVFGNPLEQARKILSYQNTYRVFYTGENEVPNFNLFDYAI 157

FILKORYKI ILHSNPNEPSDLVFGNPLEQARKI LSYQNTKRVFYTGENEVPNFNLFDYAI

49

217 168

158 GFDELDFNDRYLRMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCAL

GPDELDFNDRYLRMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCAL

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termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucosyltransferase polynori. This enzyme catalyzes the transfer of a fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein. Note: The present sequence is the SEQ ID No: 22 which is shown in the example 4 (figure 21) of the specification. This sequence differs from the SEQ ID NO: 22 given in the sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides alpha-1,3/4-fucosyltransferase (also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson KF, Bezila DJ;
                                                                         Misc-difference 414. .415
/note= "Encoded by TGATGA"
                                      'note= "Encoded by TGA"
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                                                                 'note= "Encoded by
                                                                                                                     note= "Encoded by
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note= "Encoded
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                                                                                                       .422
                                                                                                       Misc-difference 421.
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 Misc-difference 396
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                                                      Misc-difference
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(UYAL-)
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The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complexes of protein-protein interactions in Helicobacter pylori, inl for identifying modulating compounds for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                   Protein-protein interaction; ulcer; selected interacting domain; SID
                                                                                                                                                                                                                                                         Helicobacter pylori selected interacting domain (SID) protein #1601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 14.9%; Score 68; DB 5; L. Similarity 100.0%; Pred. No. 7.8e-60; 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Reuse H,
                                                                                                                                                                    Ź
                                                                        QYKFNLCFENSQGYGYVTEKI 298
                                                             OYKFNICFENSOGYGYVTEKI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 479; 642pp; English
                                                                                                                                                                 ABU52257 standard; protein; 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colland F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent an illegible residue
                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-2001; 2001WO-EP015428.
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(INSP ) INST PASTEUR
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                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
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Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ulcers in mammals.
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                                                                                                                                                                                                                                                                                                                                                 WO200266501-A2.
                                                                                                                                                                                                                             07-MAY-2003
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                                                             229
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                                                                                                                                     RESULT 4
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225 EFLSQYKFULCFENSQCYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284

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Gaps

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44.1%; Score 201; DB 9; Length 559; ilarity 100.0%; Pred. No. 8.8e-195; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 201; Conserval

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The invention relates a purified transmembrane segment-free alpha 1,3-
fucosyltransferase polypeptide, having a repeat of the sequence: X_1-X_2-
Leu-Argor_X 3-x 4-Tyr, where X 1, X_2 and X 4 is Asp or Asn; and X 3 is
Leu-Argor_X 3-x 4-Tyr, where X 1, X_2 and X 4 is Asp or Asn; and X 3 is
Leu-Argor_X 3-x 4-Tyr, where X 1, X_2 and X 4 is Asp or Asn; and X 3 is
Leu-Argor_X 3-x 4-Tyr, where X 1, X_2 and X 4 is Asp or Asn; and X 3 is
CC clie, Val or Ala. Also included are the nucleic acid encoding the protein

(including its complement or fragment), a vector containing the nucleic
acid, a host cell modified with the nucleic acid or its
comparising a host cell modified with the nucleic acid or its
comparising a host cell modified with the nucleic acid or its
contacting flucosylated oligosaccharides, such as Lex, Ley or SLex by
contacting the protein with a substrate such as Lex, Ley or SLex by
contacting the protein with a substrate, to produce oligosaccharides
and purifying the obtained oligosaccharides, or by culturing the cell,
contacting the host cell with a substrate, to produce oligosaccharides
and purifying the obtained oligosaccharides, or by culturing the obtained oligosaccharides. The nucleic acid is useful
contacting the nucleic acid using polymerase chain reaction (FCR). The
nucleic acid probe that hybridises to alphal,3-fucosyltransferase
polymucleotide, and detecting hybridisation of the probe; or by
muplifying the nucleic acid using polymerase chain reaction (FCR). The
host cell is useful for producing a transmembrane segment-free alphal,3-
fucosyltransferase-fusion protein, by growing the host cell containing a
vector operably linked to a polynucleotide encoding a desired polypeptide
cor peptide under conditions which allow expression and secretion of the protein in the
sample is indicative of infection by Helicobacter pylori or the presence
of malignant cells. The antibody is also useful for laphal,3-
fucosyltransferase gene produce and for inhibiting advantant and suring
fucosyltransferase gene prod
221 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 280
                                                                                                                                                                                                                                                                                                                                                                                                                 Enzyme; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley; sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                                                                                                                                                                                                                                                      H. pylori alphal, 3 fucosyltransferase #5.
                                                                                                                                                                                                        ABG30885 standard; protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori; strain 26695B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 6; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-00092315
                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                           285 FDEAIDYI 292
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21-OCT-2002
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This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (PutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of glycoconjugates. The present invention describes how bacterial fucosyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 26695 FutA protein sequence of the invention.
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                            228 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
the protein or cell are useful in the development of assays to detect mammalian tumours. The present sequence represents an H. pylori alphal, 3 fucosyltransferase encdoed by the fucT gene. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                        225 RFLSQYKFNLCFENSQGYGYVTEXILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Puth, FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     ;
0
                                                                                                                                              Length 424;
                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori strain 26695 FutA protein SeqID 12.
                                                                                                                                            14.9%; Score 68; DB 5; L. 100.0%; Pred. No. 7.9e-60; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ77820 standard; protein; 425 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-2003; 2003WO-US023057.
                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                  285 FDEAIDYI 292
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N-PSDB; ADJ77819.
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                                                                                                             Sequence 424 AA;
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Sequence 425 AA;

fucosyltransferase gene regulation. Oligosaccharides synthesised using

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termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycoligids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 EFLSQYKFULCFENSQGYGYYTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                                                                  Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzyme; fucT; alphal,3 fucosyltransferase; oligosaccharide; Lex; Ley; sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides alpha-1,3/4-fucosyltransferase (also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 68; DB 9; Length 425
100.0%; Pred. No. 8e-60;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bezila DJ
                                                                                                                                                                                                                        Fucosyltransferase; protein production; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. pylori alphal, 3 fucosyltransferase #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 12; 97pp; English
                                                                           AEB70141 standard; protein; 425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG30884 standard; protein; 476 AA.
                                                                                                                                                                                                                                                            Helicobacter pylori; strain 26695.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEOS-) NEOSE TECHNOLOGIES INC. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2004; 2004US-00764212
                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simala-Grant J, Taylor D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 FDEAIDYI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDEAIDYI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-521417/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AEB70140
                                                                                                                                                                                                                                                                                                US2005164338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 425 AA;
                                                                                                                                                 06-OCT-2005
                                                                                                                                                                                                                                                                                                                                    28-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2003
21-OCT-2002
                                                                                                             AEB70141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG30884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                       RESULT 8
AEB70141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG30884
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                                                                           225 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
                                                                                                             287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated alycoprotein. The method involves contacting a recombinant fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a sylycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate to the sylvoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing fucosylated glycoprotein, by contacting recombinant fucosyltransferase protein with mixture comprising donor substrate and acceptor substrate on glycoprotein.
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
                                         ö
14.9%; Score 68; DB 8; Length 425; 100.0%; Pred. No. 8e-60; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 8;
Pred. No. 8e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Scor.
100.0%; Pred. No. co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori; strain 26695FutA.
                                                                                                                                                                                                                                                                               ADJ27355 standard; protein; 425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 6; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Alpha-1,3/4-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2002; 2002US-0398156P.
08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2003; 2003WO-US023155.
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                       68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson KF, Bezila DJ;
                                                                                                                                                   285 FDEAIDYI 292
                                                                                                                                                                                  288 PDEAIDYI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDEAIDYI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDEAIDYI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-132958/13.
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADJ27354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  fucosyl; fucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004009793-A2
                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
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                                                                                                             228
                                                                                                                                                                                                                                                                                                                     ADJ27355;
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     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                          Local
                      Best Loca
Matches
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Matches
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Gaps

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Length 425;

AEB70145 standard; protein; 446 AA.

RESULT 10

AEB70145;

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Helicobacter pylori; strain 26695A
x_0
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The invention relates a purified transmembrane segment-free alpha 1,3
Eucosyltransferase polyseptide, having a repeat of the sequence: X 1-X 2
Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is

Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is

Ile, Val or Ala. Also included are the muclaic acid encoding the protein

C (including the complement or fragment), a vector containing the nuclaic

acid, a host cell containing nuclaic acid or vector, an antibody which

selectively binds to the protein and a gene expression system for

comprising a host cell modified with the nuclaic acid or its

comprising a host cell modified with the nuclaic acid or its

comprising the protein with a substrate such as Lex, Ley or Slex, by

contacting the protein with a substrate, to produce oligosaccharides

contacting the protein with a substrate, to produce oligosaccharides

and purifying the obtained oligosaccharides. The nuclaic acid is useful

contacting the bott and electing of the probe; or by

any proble for detecting the nuclaic acid, by contacting the cult of probe that hybridises to alphai, 3-fucosyltransferase

and purifying the nuclaic acid using polymerase chain reaction (PCR). The

contacting the nuclaic acid using polymerase chain reaction (PCR). The

nuclaic acid probe that hybridises to alphai, 3-fucosyltransferase

contacting the nuclaic acid using polymerase chain reaction (PCR). The cost protein and isolating the fusion protein. The probe; or by

amplifying the nuclaic acid using polymerase chain reaction (PCR) amplifying the nuclaic acid using polymerase chain reaction (PCR) amplifying the protein in a sample. The presence of the protein in the custom protein and alsolating the fusion protein. The antibody is also useful for damplant calls. The antibody is also useful for diagnosing disorders and monitoring disease, and for inhibiting abnormal alphai, 3
contacting the protein in a sample and protein creating the fusion protein or call are useful in the development of Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides. Example 3; Fig 6; 37pp; English. 98US-00092315 37-DEC-2000; 2000US-00733524 UYAL-) UNIV ALBERTA PI; 2002-582480/62 Ge Z; Sequence 476 AA; US2002068347-A1. 05-JUN-1998; 06-JUN-2002 'aylor DE,

Gaps 14.9%; Score 68; DB 5; Length 476; 100.0%; Pred. No. 8.8e-60; tive 0; Mismatches 0; Indels Conservative Local Similarity 68; Query Match Best Loca Matches ઠે

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225 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                           Helicobacter pylori fucosyl transferase, PutB, protein, SEQ ID NO: 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori fucosyl transferase, FutA, protein fragment, SEQ ID NO: 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPK 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.0%; Score 50; DB 9; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson KF, Bezila DJ;
                                                                                        Fucosyltransferase; protein production; enzyme.
                                                                                                                                                                                                                                                                       /note= "Encoded by AG"
                                                                                                                                                                              /note= "Encoded by GC"
                                                                                                                                                                                                           /note= "Encoded by AG"
                                                                                                                                                                                                                                         'note= "Encoded by AG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 16; 97pp; English.
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEB70195 standard; protein; 391 AA
                                                                                                                    Helicobacter pylori; strain 1111.
                                                                                                                                                                                                                                                                                                                                                                                                                         (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                               22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simala-Grant J, Taylor D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2005 (first entry)
                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-521417/53.
                                                                                                                                                                 Misc-difference 168
                                                                                                                                                                                               Misc-difference 355
                                                                                                                                                                                                                             Misc-difference 408
                                                                                                                                                                                                                                                       Misc-difference 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AEB70144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 446 AA;
                                                                                                                                                                                                                                                                                                      US2005164338-A1
                               06-OCT-2005
                                                                                                                                                                                                                                                                                                                                   28-JUL-2005
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This invention relates to novel isolated polynucleotides and the encoded polypeptides thereof, which are related to the fucosyltransferase enzymes (Puth and FutB) of Helicobacter pylori (H. pylori). Specifically, it refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to chemically synthesise glycoproteins and glycolipids with the desired oligosaccharide moieties (i.e. by transfer of a fucose residue to N-acetylglucosamine), such that they are useful in the preparation of altocoyltransferase is unaffected by the sialyation status of the acceptor sugar, as opposed to the mammalian homologue, and furthermore, bacterially expressed enzymes offer a large cost saving relative to mammalian expression systems. This polypeptide sequence is an H. pylori strain 1111 PutA protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an alpha-1,3/4-fucosyltransferase protein which was used in the method of the invention for producing a fucosylated
                                            New isolated polynucleotide encoding fucosyltransferase protein, useful for synthesizing oligosaccharide moiety on a protein or lipid that is unglycosylated in its native form or for synthesizing glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contacting recombinant comprising donor substrate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 DAYFSHTIPIXWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 297
                                                                                                                                                                                                                                                                                                                                                                                                       Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 8; LA
Pred. No. 1.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Scor. No. 100.0%; Pred. No. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing fucosylated glycoprotein, by c
fucosyltransferase protein with mixture
acceptor substrate on glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori; strain 1111 FutA.
                                                                                                             Claim 16; SEQ ID NO 4; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ27347 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-1,3/4-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2003; 2003WO-US023155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson KF, Bezila DJ;
WPI; 2004-123401/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-132958/13.
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADJ27346.
              N-PSDB; ADJ77811
                                                                                                                                                                                                                                                                                                                                                                         Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004009793-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fucosyl; fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ27347;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polynucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase catalytic domain (amino acids 27-417) protein fragment.
                                                                                                                                                                                                                                                                                                                         New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid; fucose; N-acetylglucosamine; glycoconjugate; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 46; DB 9; Length 391; 100.0%; Pred. No. 1.6e-37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori strain 1111 FutA protein SeqID 4.
                                                                                                                                                                                                                                                           Bezila DJ;
                  Pucosyltransferase; protein production; enzyme..
                                                                                                                                                                                                                                                           Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 66; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ77812 standard; protein; 432 AA
                                              Helicobacter pylori; strain 1111.
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                                                                                                                                                                                                            NEOSE TECHNOLOGIES INC
                                                                                                                                               22-JAN-2004; 2004US-00764212.
                                                                                                                                                                              22-JAN-2004; 2004US-00764212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-2002; 2002US-0398156P. 08-NOV-2002; 2002US-0424894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2003; 2003WO-US023057.
                                                                                                                                                                                                                                                           Simala-Grant J, Taylor D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Conservative
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                                                                                                                                                                                                                           UNIV ALBERTA
                                                                                                                                                                                                                                                                                           WPI; 2005-521417/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 391 AA;
                                                                              US2005164338-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004009838-A2
                                                                                                             28-JUL-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ77812;
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                                                                                                                                                                                                            (NEOS-)
                                                                                                                                                                                                                           (UYAL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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Gaps

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us-10-764-212-20.011g.rag

RESULT 15

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The present invention provides alpha-1,3/4-fucosyltransferase (also termed as fucosyltransferase) proteins and nucleic acids from various strains of Helicobacter pylori. This enzyme catalyzes the transfer of a fucose residue from a donor substrate to an acceptor substrate. The fucosyltransferase polymucleotides and polypeptides are useful for the synthesis of oligosaccharides, glycoproteins and glycolipids. The present sequence is Helicobacter pylori fucosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated fucosyltransferase polynucleotides and polypeptides, useful for synthesizing oligosaccharides, glycoproteins, or glycolipids.
          fucosyltransferase protein with a mixture comprising a donor substrate which comprises a fucosyl residue, and an acceptor substrate on a glycoprotein, under conditions such that the fucosyltransferase protein catalyzes the transfer of the fucose residue from a donor substrate to the acceptor substrate on the glycoprotein. The method is useful for producing fucosylated glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori fucosyl transferase, FutA, protein, SEQ ID NO: 4.
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                           251 DAYESHTIPIYWGSPSVAKOFNPKSFVNVHDFNNFDEAIDYIRYLH 296
The method involves contacting a recombinant
                                                                                                                                                                      Length 432;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simala-Grant J, Taylor D, Johnson KF, Bezila DJ;
                                                                                                                                                                                                            ö
                                                                                                                                                                      10.1%; Score 46; DB 8; Le
100.0%; Pred. No. 1.8e-37;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fucosyltransferase; protein production; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 4; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                   AEB70133 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori; strain 1111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV ALBERTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005164338-A1.
                                                                                                                                       Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-2005
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                                                                                                                                                                                                                                                                                                                                                                                                     AEB70133;
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The invention relates a purified transmembrane segment-free alpha 1,3-
tucosyltransferase polypeptide, having a repeat of the sequence: X 1-X_2-
Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
Leu-Arg-X 3-X 4-Tyr, where X 1, X 2 and X 4 is Asp or Asn; and X 3 is
C (including its complement or fragment), a vector containing the mucleic
acid, a host cell containing mucleic acid or vector, an antibody which
selectively binds to the protein and a gene expression system for
producing transmembrane segment-free alpha 1, 3- fucosyltransferase,
comprising a host cell modified with the nucleic acid or its
comprising a host cell modified with the nucleic acid or its
producing fucosylated oligosaccharides, such as Lex, Ley or Slex, by
contacting the protein with a substrate such as Lex, Ley or Slex, by
contacting the bost cell with a substrate, to produce oligosaccharides
contacting the host cell with a substrate, to produce oligosaccharides
contacting the bottained oligosaccharides. The nucleic acid is useful
contacting the obtained oligosaccharides or by
contacting the obtained oligosaccharides or by
contacting the nucleic acid using polymerase chain reaction (PCR). The
nucleic acid probe that hybridiase to alpha1,3-fucosyltransferase
contacting the nucleic acid using polymerase chain reaction (PCR). The
nost cell is useful for producing a transmembrane segment-free alpha1,3-
copyltransferase-fusion protein. by growing the host cell containing a
cvector operably linked to a polyuciceoring the presence of the protein in a sample. The presence of malliant cells. The antibody is also useful for discontant of infection by Helicobacter pylorior or the protein in a sample. The presence of malliant cells. The antibody is also useful for discontance and for inhibiting abnormal alpha1,3-
contacting the protein in a supplemental or sample contained to a roll are useful i
                                                                                                                                                                                                             Enzyme, fucT, alphal,3 fucosyltransferase, oligosaccharide, Lex; Ley;
sLex; Helicobacter pylori infection; malignant cell; mammalian tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purified transmembrane segment-free alphal, 3-fucosyltransferase polypeptide useful for producing fucosylated oligosaccharides.
                                                                                                                                                                  H. pylori alphal, 3 fucosyltransferase #7.
                    ABG30887 standard; protein; 454 AA.
                                                                                                                                                                                                                                                                             Helicobacter pylori; strain 11637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 6; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000; 2000US-00733524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00092315
                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-582480/62.
                                                                                                                                                                                                                                                                                                                        JS2002068347-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1998;
                                                                                                    29-AUG-2003
21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         raylor DE,
                                                              ABG30887;
4BG30887
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Sequence 454 AA;

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Gaps

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10.1%; Score 46; DB 9; Length 432; 100.0%; Pred. No. 1.8e-37; ive 0; Mismatches 0; Indels

Local Similarity 100. nes 46; Conservative

Matches

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Sequence 432 AA;

Query Match

DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 297

251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIRYLH 296

ö 0; Gaps Query Match 9.0%; Score 41; DB 5; Length 454; Best Local Similarity 100.0%; Pred. No. 2.2e-32; Matches 41; Conservative 0; Mismatches 0; Indels

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Search completed: August 11, 2006, 20:00:02 Job time : 121.966 secs

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OM protein - protein search, using sw model

Run on:

August 11, 2006, 20:00:25; Search time 21.4069 Seconds (without alignments) 2049.570 Million cell updates/sec

US-10-764-212-20

456 1 MPQPILIDAFIDSTHLDETTH.....TSFKIYRKAYQKSLPLLRAI 456 Title: Perfect score: Sequence:

283416 segs, 96216763 residues OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

Searched:

Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		rucosyltransierase	>	alpha (1,3)-fucosy		hypothetical prote	DNA polymerase hom	conserved hypothet	ZK112.7 protein -	hypothetical prote	major merozoite su	probable pyrophosp	large conductance	u	glycoprotein, 190K	probable nucleotid	hypothetical prote		hypothetical prote	Q.	anthranilate synth	endopeptidase-rela	hypothetical prote		hypothetical prote	two-component resp	ŏ	glycoprotein 185 -	hypothetical prote	
SUMMARIES	ID		C6456/	C64601	B71914	G71862	G83712	S39814	H70414	S44887	T10336	A43854	AC0264	F75276	PQ0125	803290	C97249	B90131	E82457	H97620	AG2843	G64329	B75359	E84078	T22314	T47706	C69859	B24796	A25814	277	D70818
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di	Query Match		٠	14.9	8.6	8.3	1.8	1.8	1.8	1.8	1.5	٠	1.5	•	٠	٠	٠	٠	٠	1.5	٠	٠	٠	•	•	1.5	٠	٠	1.5	٠	1.5
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glycerol-3-phospha	glycerol-3-phospha	glyceraldehyde-3-p	iron(III)-binding	hypothetical prote	hypothetical prote	glyceraldehyde-3-p	hypothetical prote	glyceraldehyde-3-p	hypothetical prote	glyceraldehyde-3-p	F13K23.15 protein	multidrug resistan	glyceraldehyde-3-p	tryptophan permeas
H71876	A64640	A24430	AG3582	AC2601	T23311	DEUTIC	D97383	B24430	T32555	JQ1285	F86262	B84060	DEPMINA	C44038
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312	312	336	338	354	357	359	364	385	392	396	399	401	405	417
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30	31	3 2	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1
	C64567
	fucosyltransferase - Helicobacter pylori (strain 26695)
	C;Species: Helicobacter pylori
	C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
	C;Accession: C64567
_	R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
_	Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne)
_	son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
_	Nature 388, 539-547, 1997
	A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
	A, Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
	A; Reference number: A64520; MUID: 97394467; PMID: 9252185
	A; Accession: C64567
	A; Status: preliminary; nucleic acid sequence not shown; translation not shown
_	A; Molecule type: DNA
	A;Residues: 1-425 <tom></tom>
	A;Cross-references: UNIPROT:025142; UNIPARC:UP100000D70CA; GB:AE000554; GB:AE000511; NID:
	Query Match 14.9%; Score 68; DB 2; Length 425;
	l Similarity 100.0%; Pred. No. 1.4e-63;
_	Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	ZZZ BETEGETER TOTAL TOTA
	Db 228 BFLSQYKFNLCFENSQGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
	AND THE TANK THE TANK

285 FDEAIDYI 292 |||||||| 288 FDEAIDYI 295 ઠે 셤

fucosyltransferase - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004
C;Accession: C64601
R;Accession: C64601

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-476 <TOM> A;Cross-references: UNIPROT:O25366; UNIPARC:UPI00000D70CB; GB:AE000578; GB:AE000511; NID:

Query Match

DB 2; Length 476; 14.9%; Score 68;

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A;Residues: 1-764 <AQF>
A;Cross-references: UNIPROT:O67347; UNIPARC:UPI00000565BC; GB:AE000734; GB:AE000657; NID:
A;Experimental source: strain VF5
                                                                           R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83712
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-289 <DOH>
A;Cross-references: UNIPROT:Q36545; UNIPARC:UPI000008F158; EMBL:X74132; NID:g439279; PIDN
A;Experimental source: strain Halo; etiolated shoots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
                                                                                                                                                                                                                                                                             A;Residues: 1-74 -CSTO>
A;Cross-references: UNIPROT:Q9KFH6; UNIPARC:UPI00000C38D5; GB:AP001508; GB:BA000004; NID:
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: 339814
R;Dohmen, G.; Tudzynski, P.
Curr. Genet. 25, 59-65, 1994
A;Title: A DNA-Dolymerase-related reading frame (pol-r) in the mtDNA of Secale cereale.
A;Reference number: $39814; MUID:94363738; PMID:8082167
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein aq_1328 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H70414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase homolog pol-r - rye mitochondrion (strain Halo)
C;Species: mitochondrion Secale cereale (rye)
A;Variety: strain Halo
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 289;
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Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 QNAYLDML 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Genome: mitochondrion C; Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PIDSTHLD 16
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                                                            C; Accession: G83712
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                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
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C;Species: Helicobacter pylori
A;Variety: strain J99
G;Date: 12-Peb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71862
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; i rves, C.; Gibson, R., Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.P.; A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
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X;Residues: 1-436 <ARN.
A;Cross-references: UNIPROT:Q9ZKD7; UNIPARC:UP100000D36D2; GB:AE001528; GB:AE001439; NID
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                         alpha (1,3)-fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
G;Decies: Helicobacter pylori
C;Decies: Helicobacter pylori
C;Decies: Helicobacter pylori
C;Decies: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004
C;Accession: B71914
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; inves, C.; Gibson, R., Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.P.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A1800; MUID:99120557; PMID:9923662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .Cross-references: UNIPROT:09ZLI3; UNIPARC:UPI00000D3665; GB:AE001491; GB:AE001439; NII
Experimental source: strain J99
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                                                                                                                               228 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287
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G83712
hypothetical protein BH0503 [imported] - Bacillus halodurans (strain C-125)
                                                                                          225 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDF 115
      Best Local Similarity 100.0%; Pred. No. 1.6e-63; Matches 68; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 8.9e-33;
iive 0; Mismatches 0;
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100.0%; Pred. No. 9.8e-32;
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Best Local Similarity 100.0
Matches 39; Conservative
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                    288 FDEAIDYI 295
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C. Accession: Acozet
R. Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I.
Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; WUID:21470413; PMID:11586360
                  C;Accession: A43854
R;Hui, G.S.; Hashimoto, A.; Chang, S.P.
Infect. Immun. 60, 1422-1433, 1992
A;Title: Roles of conserved and allelic regions of the major merozoite surface protein (c A;Reference number: A43854; MUID:92192814; PMID:1548068
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; J. M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma)
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A;Cross-references: UNIPROT:Q9RRR4; UNIPARC:UP100000D3FB5; GB:AE002072; GB:AE000513; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A,Modecule type: DNA
A;Readues: 1-128 <br/>KUIR>
A;Cross-references: UNIPROT:Q8ZEJ8; UNIPARC:UPI0000DCA34; GB:AL590842; PIDN:CAC90975.1;
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Cispecies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Residues: 1-89 <HUI>
A;COSB-references: UNIPARC:UPI0000177F83
A;CrosB-references: UNIPARC:UPI0000177F83
A;Experimental source: FVO isolate
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:89242, NCBIP:89243)
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100.0%; Pred. No. 24;
tive 0; Mismatches
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Matches 7; Conservative
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appearated to the EMBL Data Library, May 1993
A; Description: Sequence of the C. elegans cosmid ZK112.
A; Reference number: S44616
A; Reference number: S44887
A; Accession: S44887
A; A; Status: preliminary
A; Residues: 1-3343 < DUZ>
A; Residues: 1-3343 < DUZ>
A; Cross-references: UNIPROT: P34616; UNIPARC: UPI000013BC7C; EMBL: L14324; NID: 9289740; PID
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R;Abrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
R;Abrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
A;Irioley 229, 381-399, 1997
A;Title: Asquence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10336
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major merozoite surface protein gp195 - malaria parasite (Plasmodium falciparum) (fragme
C;Species: Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: 010321; UNIPARC: UPI000066182F; EMBL: U75930; NID: 92934903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S44887
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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                              AjGene: aq_1328
C;Superfamily: Aquifex aeolicus conserved hypothetical protein aq_1328
C;Keywords: App; nucleotide binding; P-loop
F;70-77/Region: nucleotide-binding motif A (P-loop)
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100.0%; Pred. No. 15;
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100.0%; Pred. No. 12;
tive 0; Mismatches
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100.0%; Pred. No. 47;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-79 < AHR>
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Search completed: August 11, 2006, 20:09:13 Job time : 25.4069 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-138 <KIM>
A;Residues: 1-138 <KIM>
A;Crestences: UNIPROT:Q25960; UNIPARC:UP10000082067; GB:M32116; NID:g160502; PIDN:
C;Superfamily: G surface protein
C;Reywords: glycoprotein; surface antigen
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XResidues: 1-146 <SCH.
A;Cross-references: UNIPROT:Q8T6A9; UNIPROT:Q9TZV2; UNIPROT:Q9TZU9; UNIPARC:UPI0000177F8
C;Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S03290
R;Scherf, A.; Barbot, P.; Langeley, G.
Rucleic Acids Res. 17, 1744, 1989
A;Title: Sequence and length polymorphism of a major malaria vaccine candidate analysed A;Reference number: S03290; MUID:89160345; PMID:2646601
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A,Variety: isolate Bandia-Senegal
C,Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
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100.0%; Pred. No. 28;
tive 0; Mismatches
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A;Status: translation not shown
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Best Local Similarity 100.
Matches 7; Conservative
                   A;Map position: 1
C;Superfamily: yhdC protein
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A;Gene: DR2422
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                        A;Accession: C97249
A;Status: preliminary
A;Molecule: trype: DNA
A;Residues: 1-152 <NUR
A;Cross-references: UNIPROT:Q97FA2; UNIPARC:UP100000CA65A; GB:AE001437; PIDN:AAK80782.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
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C;Superfamily: ATPase likely involved in cell wall biosynthesis
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61 SNPNEPSDLVFGNPLEQARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDFNDRYL 120
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Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=2013842; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
MESLINE=2013842; PubMed=10671538; DOI=10.1074/jbc.275.7.4988;
MESKO D.A., Wang G., Palcic M.M., Taylor D.E.;
"Cloning and characterization of the alpha(1,3/4) fucosyltransferase
                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF194963; AAF35291.2; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:tucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
GO; GO:0016486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco trans 10.
PANTHER; PTHR1929; Glyco_trans 10.
Glycosyltransferase; Transferase.
SEQUENCE 462 AA; 54560 MW; BD27F8BB35IBCE752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rasko D.A., Wang G., Palcic M.M., Taylor D.E.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 456; I
                                                                                                                                                                                                                                                                                                                                                                                                                                   of Helicobacter pylori.";
J. Biol. Chem. 275:4988-4994(2000).
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                                                                  August 11, 2006, 19:54:19 ; Search time 160.721 Seconds
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1 MFQPLLDAFIDSTHLDETTH.....TSFKIYRKAYQKSLPLLRAI
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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Q7XYL3_CRYPO
Q36545_SECCE
Q368C1_9GAMM
Q7Q403_ANOGA
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032631 HELPY
092K13 HELPU
092K07 HELPU
090511 HELPY
09FDN3 BACFR
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Q99CBO_BRAJA
Q9KFH6 BACHD
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Length 462; Indels

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		462 AA.	PRT; 4	JRY;	PRELIMINARY;		T 1 4 HELPY 09L8S4 HELPY	RESULT 1 Q9L8S4 HELPY ID Q9L8S4
		NTS	ALIGNMENTS					
sr6 shewanella	Q2zsr6	Dd	Q2ZSR6_SHEPU	0	3 509	1.8	ထ	45
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nh9 methanosarc	OBtmb9	AC A	OSTMH9 METAC	4 (	497		0 00	1 4 2 E
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	Q8trx0	AC	Q8TRX0_METAC	~	3 494	1.8	æ	40
_	Q8pxp4	ΨA	Q8PXB4_METMA	7		1.8	æ	39
ly6 methanosarc	08puy6	ΜA	Q8PUY6_METMA	~	3 494	1.8	<b>α</b> ο	38
ii9 methanosarc	08pui9	MA	Q8PUI9 METMA	7		1.8	æ	37
-	Q8evs9	PE	Q8EVS9 MYCPE	7		1.8	æ	36
	Q3wda9	5 P	Q3WDA9 9ACTO	7	3 421	1.8	æ	35
-	085176		ASSY CORGL	н		1.8	80	34
	Q4jvz8	¥	Q4JVZ8 CORJR	7		1.8	æ	33
	Q8tmt6	AC	QBTMT6_METAC	7		<u>-</u>	80	32

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=26695 / ATCC 700323.
STRAIN=26695 / ATCC 700323.
Tomb J.-F., White O., Kerlawage A.R., Clayton R.A., Sutton G.G., Feleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Bleischmann R.D., Ketchum K.B., Quackenbush J., Zhou L., Kirkness E.F., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Heterson S.N., Loftus B.J., Richardson D.L., Dodon R.J., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Watthey J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Ebrodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN
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Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                             OrderedLocusNames=HP0379; ORFNames=HP_0379;
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016717; F:transferase activity, transferring glycosyl...
GO; GO:0016717; F:transferase activity, transferring glycosyl...
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans_10.
INTER; PTHR11929; Glyco_trans_10; I.
PANTHER; PTHR11929; Glyco_trans_10; I.
COMplete proteome; Glycosyltransferase; Transferase.
SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.9%; Score 68; DB 2; Length 425; Best Local Similarity 100.0%; Pred. No. 7.5e-60; Matches 68; Conservative 0; Mismatches 0; Indels
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=26695 / ATCC 700392;
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                                                                11-JAN-1998, integrated into UniProtKB/TrEMBL
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PIR; C64567; C64567.
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07-FEB-2006, entry version 24.
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   121 RMPLYYAYLHYKAMLVNDTTSPYKLKALYTLKKPSHKFKENHPNLCALIHNESDPWKRGF 180
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                                                                                                                                                                                                                                         241 GYGYVTEKILDAYPSHTIPIXWGSPSVAKDFNPKSFVNVHDFNNPDEAIDYIRYLHAHQN
                                                                                                                                                                                                                                                                                                                                                                  301 AYLDMLYENPLNTIDGKAGFYQDLSFEKILDFFKNILENDTIYHCNDAHYSALHRDLNEP
                                                                      ASFVASNPNAPIRNAFYDALNAIBPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFENSQ
                                                                                                        181 ASFVASNPNAPIRNAFYDALNAIEPVASGGSVKNTLGYKVKNKNEFLSQYKFNLCFENSQ
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"Molecular Cloning and Functional Expression of a Novel Helicobacter pylori {alpha}-1,4 Fucosyltransferase.";
Glycobiology 15:1076-1083(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016417; F:fucosyltransferase activity; IEA.
GO; GO:0016486; F:transferase activity, transferring glycosyl.
GO; GO:0016486; F:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTR411929; Glyco_trans_10;
BANTHER; PTR411929; Glyco_trans_10;
Glycosyltransferase; Transferase.
SEQUENCE 432 AA; SO503 MW; 69D3A32FBD2F12C9 CRC64;
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PubMed=16000696; DOI=10.1093/glycob/cwj004;
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MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016757; F:transferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0006486; F:protein amino acid glycosylation; IEA.
InterPro; IPR01503; Glyco_trans_10.
PANTHER; PTR11929; Glyco_trans_10; 1.
COMplete proteome; Glycosyltransferase.
COMplete proteome; Glycosyltransferase.
SEQUENCE 476 AA; 55527 PM; 32BFPDBBD36E174 CRC64;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008417; F:fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0006486; P:protein amino acid glycosylation; IEA.
                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Bougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftens B.J., Richardson D.L., Dodson R.J., Khalak H.G. Glodek A., McKenney K., PitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.P., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
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01-JAN-1998, sequence version 1.
07-FRE-2006, entry version 23.
Alpha (1,1)-fucosyltransferase (EC 2.4.1.-).
Name-fucT;
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Lewis X biosynthesis in Helicobacter pylori. Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NCTC 11637;
MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
MEDLINE=97407924; PubMed=9261148; DOI=10.1074/jbc.272.34.21349;
Bird M.I.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.9%; Score 68; DB 2; Length 476; 100.0%; Pred. No. 8.3e-60; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 AA.
                                                                                                                                                                                                                                                                                                   EMBL; AE000511; AAD07710.1; -; Genomic_DNA.
PIR; C64601; C64601.
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J. Biol. Chem. 272:21349-21356(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O32631 HELPY PRELIMINARY;
032631;
                                                                                                                                                                                                         Nature 388:539-547(1997).
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288 FDEAIDYI 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038146495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., Garge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                         01.MAY-1999, sequence version 1.
21-FEB-2006, entry version 23.
ALPHA (1,3)-FUCCSYLTRANSFRASE.
Name=fucT; ORFNames=jhp_0596;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria: Epsilonproteobacteria; Campylobacters; Helicobacteraes; Helicobacteraes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BioCyc; HPYL8563:JHP0596-MONOMER; -. GO; GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:0008417; F:transferase activity, transferring glycosyl. GO; GO:0016757; F:transferase activity, transferring glycosyl. GO; GO:0016486; P:protein amino acid glycosylation; IEA. GO; GO:0016486; P:protein amino acid glycosylation; IEA. PANTHER; PTHR11929; Glyco_trans 10; 1. Complete proteome; Glycosyltransferase; Transferase. SEQUENCE 454 AA; 53448 MW; 3262687131263AB0 CRC64:
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                                                                                                  9.0%; Score 41; DB 2; Length 333;
100.0%; Pred. No. 2e-32;
ive 0; Mismatches 0; Indels
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InterPro; IPR001503; Glyco_trans_10.
PANTHER; PTR11929; Glyco_trans_10; 1.
Glycosyltransferase; Transferase.
SEQUENCE 333 AA; 39154 MW; CFFCB1AC127E0A8C CRC64;
                                                                                                                                                                                                               132 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDY 172
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01-MAY-1999, sequence version 1.
21-FRB-2006, entry version 23.
ALPHA-(1,3)-FUCOSYTRANSFRRASE.
Name-fuctj ORFNames-jhp 1002;
Helicobacter pylori J99 (Campylobacter pylori J99).
                                                                                                                                                                                       251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDY
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8.6%; Score 39; DB 2; Lo
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 39; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                            454 AA.
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PIR; B71914; B71914.
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                41; Conservative
                                                                                                                            Local Similarity
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[1]
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Q9ZKD7_HELPJ
Q9ZKD7;
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O9ZLI3;
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Matches
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7.0%; Score 32; DB 2; Length 478;
00.0%; Pred. No. 4e-23;
ve 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.5;
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DNA-binding; Transcription; Transcription regulation.
SEQUENCE 308 AA; 35190 MW; 2A89F365C77A949F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redox-sensitive transcriptional activator OxyR
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001, integrated into UniProtKB/TrEMBL, 01-MAR-2001, sequence version 1.
                                                                                                                                        251 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 282
                                                                                                                                                                           253 DAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDF 284
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-ive 0; Mismatches
                 100.0%; Prec. ...
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MEDLINE=20416215; PubMed=10960088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry version 21
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                                                                      32, Conservative
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Matches 9; Conservative
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65 LEQARKILS 73
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       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            Q9FDN3_BACFR
Q9FDN3;
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0008417; F:fucosyltransferase activity; IEA.

GO; GO:0016797; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:0016787; F:transferase activity, transferring glycosyl. . .; IEA.

GO; GO:0006486; P:protein.amino acid glycosylation; IEA.

InterPro; IPR011509; Glyco_trans 10.

PANTHER; PTHR11929; Glyco_trans 10.

Glycosyltransferase; Transferase.

Glycosyltransferase; Transferase.

SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .; IEA.
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MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;
Ge Z., Chan N.W.C., Palcic M.M., Taylor D.B.;
"Cloning and heterologous expression of an alphal,3-fucosyltransferase gene from the gastric pathogen Helicobacter pylori.";
J. Biol. Chem. 272:21357-21363(1997).
                                                                                                                                 MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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Nature 397:176-180(1999).
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, G11862; G71862.

G0; G0:0016020; C:membrane; IRA.
G0; G0:0008417; F:fucosyltransferase activity; IEA.
G0; G0:0016757; F:transferase activity, transferring glycosyl.
G0; G0:0016757; F:transferase activity, transferring glycosyl.
G0; G0:0006486; P:protein amino acid glycosylation; IEA.
InterPro; IPR001503; Glyco_trans 10.
InterPro; IPR001503; Glyco_trans 10.
PANTHER; PTHR11929; Glyco_trans 10.
Complete protecome; Glycosyltransferase; Transferase.
SEQUENCE 436 AA; 50699 WW; IDB2066AE98FA6IE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ARKILSYQNTKRVFYTGENEVPNFNLFDYAIGFDELDF 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001439; AAD06573.1; -; Genomic_DNA.
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                                      Helicobacteraceae; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                         NCBI_TaxID=85963;
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Gaps
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HSSP; P11721; 1169.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006350; P:transcription; IEA.

InterPro; IPR0005147; HTH_LysR.

InterPro; IPR001991; Wing_hlx_DNA_bd.

Pfam; PF00126; HTH_1; 1.

Pfam; PF003466; LysR gubstrate; 1.

PRINTS; PR00039; HTHLYSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOI=10.1128/JB.182.18.5059-5069.2000;
Socha B.K., Owena G. Jr., Smith C.J.;
"The redox-sensitive transcriptional activator OxyR regulates the
peroxide response regulon in the obligate anaerobe Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QELECOR BACFN PRELIMINARY; PRT; 308 AA.
QELEQB;
21-JUN-2005, integrated into UniProtKB/TrEMBL.
21-JUN-2005, sequence version 1.
07-PEB-2006, entry version 3.
Redox-sensitive transcriptional activator.
Name-oxyR; OrderediocusNames=BF1118;
Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
Bacteria; Bacteroideces; Bacteroidetes (class); Bacteroidales;
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Bacteroidaceae, Bacteroides.
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-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
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1.8%; Score 8;
                                                                                                                                    InterPro; IPR000847; HTH LYBR.
InterPro; IPR005119; LyBR_subst_bd.
InterPro; IPR011991; Wing_hlx_DNA_bd.
Pfam; PF00126; HTH 1; 1.
Pfam; PP03466; LyBR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
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ProDom; PD007253; MS_channel; 1.
TIGRFAMB; TIGR00220; mscL; 1.
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Pfam; PF01741; MscL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 13:1572-1579(2003).
                                                                                                                                                                                                                                                     Transcription regulation. SEQUENCE 308 AA; 35248
                                                                                                                                                                                                                                                                                                                          9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               73
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Matches
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                                                     Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
Line A., Lord A., Norbertczak H., Ormond D., Price C.,
Rabbinowitsch E., Woodward J., Barrell B.G., Parkhill J.,
"Extensive DNA inversions in the B. fragilis genome control variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                              Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                    EMBL; CR626927; CAH07035.1; -; Genomic_DNA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006350; P:resulacription; IEA.
InterPro; IPR000847; HTH LysR.
InterPro; IPR000847; HTH LysR.
InterPro; IPR01991; Wing_hlx_DNA_bd.
Pfam; PF00126; HTH 1; I.
Pfam; PF00126; HTH 1; I.
Pfam; PF00126; HTH 1; I.
Pfam; PF00126; HTH 1; I.
Pfam; PF00126; HTH 1; I.
Pfam; PF00146; DNA_bd.
Complete proteome; DNA_binding; Transcription;
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DOL=10.1128/JB.182.18.5059-5069.2000;
Rocha B.R., Owens G.T., Srith C.J.;
"The redox sensitive transcriptional activator OxyR regulates the
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Bacteroidaceae; Bacteroides.
NCBL_TaxID=817;
                                                                                                                                                     Science 307:1463-1465(2005).
-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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SEQUENCE 308 AA; 35248 MW; B3AD6095FB895BA3 CRC64;
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                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15746427; DOI=10.1126/science.1107008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=YCH46;
PubMed=15466707; DOI=10.1073/pnas.0404172101;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 2;
Pred. No. 7.5;
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Local Similarity 100.0%; Pred. No. 7.5
Les 9; Conservative 0; Mismatches
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Q9FDN4;
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                                                                                                                                          gene expression.";
NCBI_TaxID=272559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                    transcription, DNA-dependent; IEA
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E. Sugimoto S., Mateui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
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07-FEB-2006, entry version 13.
Putative large-conductance mechanosensitive channel protein.
OrderedLocusNames-ECB053;
Corymebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 AA; 35248 MW; B3AD6095FB895BA3 CRC64;
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                                                                                                                                                                                                            GO; GO:0003700; P:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-de
GO; GO:0006350; P:transcription; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50931; HTH LYSR; 1.
Complete proteome; DNA-binding; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1.
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100.0%; Pred. No. 7.5;
ative 0; Mismatches
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                             EMBL; AF206033; AAG02619.1; -; Genomic_DNN.
EMBL; AP006841; BAD48083.1; -; Genomic_DNN.
HSSP; P11721; 1169.
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Length 151;

DB 2;

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RESULT 13 Q34YL2 9GA

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                      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Welsenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae; Histophilus.
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Pontarollo R.A.;
Thesis (1996), V. I. D. O., University of Saskatchewan.
MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
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GO; GO:0019069; P:viral capaid assembly; IEA.
InterPro; IPR09225; Phage GPL.
Pfam; PF05926; Phage GPL;
SEQUENCE 170 AA; I9924 MW; 9D1C2C427A5F20B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 AA; 17077 MW; 67F13D46A7C90FD3 CRC64;
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100.0%; Pred. No. 47;
tive 0; Mismatches
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100.0%; Pred. No. 44;
tive 0; Mismatches
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BioCyc; RSOL305:RSC1935-MONOMER; -.
GO; GO:0019069; P:viral capsid assembly; IEA.
InterPro; IPR092225; Phage GPL.
Pfam; PF05926; Phage GPL.
Complete profesome.
SEQUENCE 159 AA; 17077 MW; 67F13D46A7C90E
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Haemophilus somnus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 SVDDLRRD 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Larimer F., Land M.;
"Annotation of the draft genome of Alkalilimnicola ehrlichei MLHB-1.";
"Annotation of the draft genome of Alkalilimnicola ehrlichei MLHB-1.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Alkalilimnicola enrichei MLHE-1.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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QBXY28;
QBXY28;
QBXY28;
QBXY28;
QBYAR-2002, integrated into UniProtKB/TrEMBL.
O1-MAR-2002, educace version 1.
O7-FEB-2006, entry version 16.
PROBABLE BACTERIOPHAGE PROTEIN.
OrderedLocusNames=RSc1935; ORFNames=RS03504;
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Alkalilimnicola ehrlichei MLHE-1.
Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales;
Ectothiorhodospiraceae, Alkalilimnicola.
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SEQUENCE 154 Aa; 15050 MW; 85FB6AD5FBAD0384 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        06-DEC-2005, integrated into UniProtKB/TrEMBL. 06-DEC-2005, sequence version 1. Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                     154 AA.
      Pred. No. 42;
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US DOE Joint Genome Institute (JGI-ORNL);
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100.08;
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Best Local Similarity 100.
Matches 8; Conservative
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Search completed: August 11, 2006, 20:08:04 Job time : 165.721 secs

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GENERAL INFORMATION:
APPLICATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/733,524A
CURRENT APPLICATION NUMBER: US/09/2,315
PRIOR FILING DATE: 1998-06-05
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Matches 68; Conserv
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/EMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-733-524A-5

US-09-733-524A-8

US-10-189-977A-8

US-10-189-977A-8

US-10-189-977A-8

US-10-189-977A-2

US-09-733-524A-2

US-09-733-524A-2

US-09-733-524A-2

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seq length: 200000000
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US-09-893-13377
US-09-893-737-2
US-09-883-737-2
US-09-883-737-2
                                                                                                                                                                                                                               Sequence 6, Application US/09092315

Patent No. 639937
GENERAL INFORMATION:
APPLICANT: TAYLOR, Diame E.
APPLICANT: Ge, Zhongming
ITILE OF INFORTION: ALPHA-1, 3-FUCOSYLTRANFERASE
ITILE REPERRACE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SEQTHARE: FASTSEQ for Windows Version 3.0
SEQTHARE: LABSED OF WINDOWS OF SEQ ID NOS: 22
LEMETH: 425
LEMETH: 425
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100.0%; Pred. No. 2.2e-56;
trive 0; Mismatches 0;
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US-09-092-315-6
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225 BFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 284
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                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: H. pylori strain 26695B
OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
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Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels
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APPLICANT: Taylor, Diane B.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
TILE REFERENCE: 07254/049001
CURRENT PPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASELSEQ for Windows Version 3.0
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14.9%; Score 68; DB 3; L.
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 68; Conservative 0; Mismatches 0;
                                        PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1097-06-06
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1998-06-05
PRIOR PELICATION NUMBER: US 09/092,315
PRIOR PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATCHTIN VEY: 2.1
SEQ ID NO 6-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-092-315-5; Sequence 5, Application US/09092315; Patent No. 6399337; GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
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288 FDEAIDYI 295
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REPERBINGE: 0724-049002
CURRENT APPLICATION NUMBER: US/09/73A
CURRENT PILING DATE: 2002-03-07
FRIOR APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR PILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 425
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Pred. No. 2.2e-56;
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Patent No. 702991.
Barent No. 702991.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398-000420US
                                                                                                                                                                                                                                              Query Match 14.9%; Score 68; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 68; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 6
LENGTH: 425
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                                                                                                                                                ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-6
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Sequence 5, Application US/10392098A
Patent No. 7029891
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Patent No. 6399337
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
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Best Local Similarity 100.0
Matches 41, Conservative
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288 FDEAIDYI 295
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: WUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFREENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/10/189,977A
CURRENT PILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 27
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S
LENGTH: 476
TYPE: PRI
                 APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC CLIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: PUCCSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US (09/092,315
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR APPLICATION NUMBER: US 60/048,857
PRIOR APPLICATION NUMBER: US 60/048,407
PRIOR PILING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 476
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14.9%; Score 68; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-733-524A-5
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US-10-189-977A-5
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Best Local Similarity 100.u
Diane E.
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OTHER INFORMATION: H. pylori strain 26695A

OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
US-10-392-0988-5
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GENERAL INC. 702391
GENERAL INC. 702391
GENERAL INCORVATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: University of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 01738-000420US
CURRENT APPLICATION NUMBER: US/10/130,098A
CURRENT FILING DATE: 2003-03-17
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1000-12-07
NUMBER OF SEQ ID NOS: 30
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APPLICANT TAYLOR. Diane E.
APPLICANT Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRAESEQ FOR WINDOWS Version 3.0
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Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 68; Conservative 0; Mismatches 0;
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OTHER INFORMATION: H. pylori strain NCTC11637
OTHER INFORMATION: alpha-1,3-fucosyltransferase fucT (HpFucT)
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APPLICANT: Taylor, Diance E.
APPLICANT: Taylor, Diance E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/09/092,315
CURRENT APPLICATION NUMBER: US 60/048,857
EARLIER APPLICATION NUMBER: US 60/048,857
EARLIER PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                         APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
APPLICANT: Ge, Zhongming
TITLE OF Iniversity of Alberta
TITLE OF INVENTION: Alpha-1,3 Fucosyltransferase
FILE REFERENCE: 017398-000420US
CURRENT APPLICATION NUMBER: US/10/392,098A
CURRENT PILING DATE: 2003-03-17
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
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8.6%; Score 39; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 39; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e-30;
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Sequence 8, Application US/10392098A Patent No. 7029891
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09092315
Patent No. 6399337
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US-09-092-315-2
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US-09-733-524A-2
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LENGTH: 454
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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, ZANDGMING
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION NUMBER: US/09/733,524A
CURRENT FILING DATE: 1908-06-05
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
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APPLICANT: Taylor, Diane B.
APPLICANT: Taylor, Diane B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
FILE REFERENCE: 07254-049002
CURRENT APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US/09/733,524
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-06
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PastSEQ for Windows Version 4.0
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9.0%; Score 41; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0;
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9.0%; Score 41; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 41; Conservative 0; Mismatches 0;
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                                                                                                                            Sequence 8, Application US/09733524A
Patent No. 6534298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Helicobacter pylori
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US-10-189-977A-8
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US-10-189-977A-8
                                                                                      US-09-733-524A-8
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LENGTH: 454
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RESULT 12 US-10-392-098A-8

Best Loca Matches

Length 486;

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Sequence 2, Application US/10189977A

Sequence 2, Application US/10189977A

Sequence 2, Application US/10189977A

Patent No. 6962806

GENERAL INFORMATION:

APPLICANT: TAYLOT, Diane B.

APPLICANT: Ge, Zhongming

TITLE OF INVENTION: FUCOSTIFRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND

TITLE OF INVENTION: EXPRESSING THEM (amended)

TITLE OF INVENTION: EXPRESSING THEM (amended)

FILE REFERENCE: 07254-049002

CURRENT APPLICATION NUMBER: US/10/189,977A

CURRENT FILING DATE: 2000-12-07

PRIOR FILING DATE: 1990-06-05

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR APPLICATION NUMBER: US 09/092,315

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 486
                      APPLICANT: Ge, Zhongming
TITLE OF INVENTION: UCLUEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: UCCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
CURRENT APPLICATION NUMBER: US/09/733,524A
CURRENT APPLICATION NUMBER: US/09/733,524A
CURRENT FILING DATE: 2000-12-07
PRIOR PLLING DATE: 1998-06-05
PRIOR PLLING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTERE (for Windows Version 4.0)
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; ORGANISM: Helicobacter pylori
US-09-733-524A-2
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ORGANISM: Helicobacter pylori
APPLICANT: Taylor, Diane E.
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US-10-189-977A-2
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Query Match 8.6%; Score 39; DB 2; Length 486; Best Local Similarity 100.0%; Pred. No. 1.1e-28; Matches 39; Conservative 0; Mismatches 0; Indels

US-10-189-977A-2

ઠ 셤 Search completed: August 11, 2006, 20:10:49 Job time : 32.6006 secs

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Publication No. US20050164338A1
GENERAL INFORMATION:
APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Governors of the University of Alberta
APPLICANT: Governors of the University of Alberta
TILLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
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US-10-392-098-3
US-10-764-212-18
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Patent No. US20020068347A1

GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Canada Corporation

APPLICANT: Taylor, Diane B.

APPLICANT: Taylor, Diane B.

APPLICANT: G. Zhongming

TITLE OF INVENTION: FUCCOSTLTRANSFERASES AND EXPRESSION SYSTEMS FOR WAKING AND

TITLE OF INVENTION: EXPRESSING THEM

FILE REFERENCE: 07254/049002

CURRENT APPLICATION NUMBER: US/09/733,524
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                                                                                        361 LVSVDDLRRDHDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRRDHDDLRRDH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:H. pylori
OTHER INFORMATION: strain 955 FutA fucosyltransferase coding
OTHER INFORMATION: sequence amino acid translation peptide
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APPLICANT: Saylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Bezila, Daniel James
APPLICANT: Bezila, Daniel James
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
FURENT APPLICATION NUMBER: US/10/764,212
CURRENT APPLICATION NUMBER: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 44.1%; Score 201; DB 5; Le Best Local Similarity 100.0%; Pred. No. 4.2e-182; Matches 201; Conservative 0; Mismatches 0;
                                                                                                                                                       421 ERLISKATPLIELSQNTSFKIYRKAYQKSLPLIRAI 456
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                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/10764212
Publication No. US20050164338A1
GENERAL INFORMATION:
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US-10-764-212-25
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APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/120,319
CURRENT FILING DATE: 2002-04-09
FRIOR PILING DATE: BARLIER FILING DATE: 1998-06-05
PRIOR PILING DATE: BARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 425
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Pred. No. 1.3e-55;
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100.0%; Pred. No. 1.3e-55;
ative 0; Mismatches 0;
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ORGANISM: Helicobacter pylori fucosyltransferase
PEATURE:
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14.9%; Score 68; DB
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 68; Conservative 0; Mismatches
            PRIOR APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 20
SOFTMARE: PRESEQ for Windows Version 4.0
SERVING: 1424
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                                                                                                                                                                                                                                                                                                        ; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 26695B
US-09-733-524-16
2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
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Best Local Similarity
Matches 68; Conserv
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NUMBER OF SEQ ID NOS: 20
SOFWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15
LENCTH: 476
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; OTHER INFORMATION: Strain 26695A
US-09-733-524-15
                                                 Taylor, Diane
Johnson, Karl F.
Bezila, Daniel James
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Helicobacter pylori
                        APPLICANT: Simala-Grant, APPLICANT: Taylor, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 FDEAIDYI 292
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# TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

# TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

# TITLE OF INVENTION: EXPRESSING THEM (amended)

# TITLE OF INVENTION: EXPRESSING THEM (amended)

# TITLE OF INVENTION: EXPRESSING THEM (amended)

# TITLE OF INVENTION: EXPRESSING THEM (amended)

# TITLE OF INVENTION: EXPRESSING THEM (amended)

# FILE REFERENCE: 07254-04902

# CURRENT FILING DATE: 2003-03-17

# PRIOR PELICATION NUMBER: US 60/92,315

# PRIOR PELING DATE: 1998-06-05

# PRIOR PELING DATE: 1998-06-05

# PRIOR PILING DATE: 1997-06-06

# NUMBER OF SEQ ID NOS: 27

# SQFTWARE: FastSEQ for Windows Version 4.0

# SEQ ID NOS: 27

# SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                            Length 425;
                                                                                                                                                                                                                                                                                                                                     Score 68; DB 4; Length act. Pred. No. 1.3e-55;
FILLE DEFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US/09/092,315
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTESQ-for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                        ch 14.9%; Score 68; DB 1 Similarity 100.0%; Pred. No. 1.3 68; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-189-977-6
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ORGANISM: Helicobacter pylori
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Best Local Similarity 100.v
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US-10-764-212-12
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Sequence 15, Application US/09733524

Sequence 15, Application US/09733524

Batent No. US20020068347A1

GENERAL INFORMATION:
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
TITLE OF INVENTION: NUCLEIL ERFERENCES AND EXPRESSION SYSTEMS FOR MAKING AND
TITLE OF INVENTION: EXPRESSING THEM
FILE OF INVENTION: EXPRESSING THEM
TITLE OF INVENTION: EXPRESSING THEM
TITLE OF INVENTION: WIMBER: US/09/733,524
CURRENT FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 09/092,315
PRIOR APPLICATION NUMBER: 60/048,857

PRIOR APPLICATION NUMBER: 60/048,857

PRIOR APPLICATION NUMBER: 60/048,857
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14.9%; Score 68; DB 3; Length 476
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 68; Conservative 0; Mismatches 0; Indels
APPLICANT: Johnson, Karl F.
APPLICANT: Bezila, Daniel James
APPLICANT: Bezila, Daniel James
APPLICANT: Neose Technologies, Inc.
APPLICANT: Governors of the University of Alberta
TITLE OF INVENTION: H. Pylori Fucosyltransferases
FILE REFERENCE: 019957-019400US
CURRENT FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12.
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288 FDEAIDYI 295

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285 FDEAIDYI 292
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Best Local Similarity
Matches 68; Conserv
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                                                                  RESULT 11
US-10-392-098-5
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                                                                                                                        Sequence 5, Application US/10120319; Publication No. US20020164749A1; Sequence 5, Application No. US20020164749A1; Seguence 5, Application No. US20020164749A1; Seminary Information: Information: Diame E.; APPLICANT: Taylor, Diame E.; APPLICANT: Ge, Zhongming; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE; FILE REFERENCE: 07254/04901; CURRENT APPLICATION NUMBER: US/10/120,319; CURRENT FILING DATE: 2002-04-09; PRIOR APPLICATION NUMBER: RABLIER APPLICATION NUMBER: 09/092,315; PRIOR PILING DATE: BARLIER FILING DATE: 1998-06-05; PRIOR FILING DATE: BARLIER FILING DATE: 1997-06-06; NUMBER: PRESEQ for Windows Version 3.0
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APPLICANT: Ge, Zhongwing
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/04901
CURRENT APPLICATION NUMBER: US/10/189,977
CURRENT FILING DATE: 1998-06-05
FRIOR FILING DATE: 1998-06-05
FRIOR APPLICATION NUMBER: US 60/048,857
FRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRSESEQ FOR WINDOWS Version 3.0
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ORGANISM: Helicobacter pylori
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ORGANISM: Helicobacter pylori
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288 FDEAIDYI 295
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Best Local Similarity
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LENGIH: 476
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228 EFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNN 287

285 FDEAIDYI 292

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APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: EXPRESSING THEM (amended)
TITLE OF INVENTION: DATE: 1003-03-17
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 09/092,315
PRIOR APPLICATION NUMBER: US 00/048,857
PRIOR APPLICATION NUMBER: US 00/048,857
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASKESQ for Windows Version 4.0
SEQ ID NO S: 27
SEQ ID NO S: 27
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SERVICE ACIDE OF TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXLORD THE TAXL
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; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Taylor, Diane
; APPLICANT: Recard Technologies, Inc.
; APPLICANT: Rece Technologies, Inc.
; APPLICANT: Governors of the University of Alberta
; TITE OF INVENTION: H. Pylor: Rucosyltransferases
; TITE REPERENCE: 019957-019400US
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 16
; SEQ ID NO 16
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11.0%; Score 50; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 1.7e-38;
Matches 50; Conservative 0; Mismatches 0;
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; Sequence 5, Application US/10392098; Publication No. US20030166212A1; GENERAL INFORMATION:
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Search completed: August 11, 2006, 20:16:18
Job time : 111.092 secs
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LENGIH: 454
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OTHER INFORMATION: catalytic domain conserved region positions 27-417
227 BFLSQYKFNLCFENSQSYGYVTEXILDAYFSHTIPIYWGSPSVAKDFNPK 276
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; Publication No. US20050164338A1
; GENERAL INFORMATION:
; APPLICANT: Simala-Grant, Joanne
; APPLICANT: Taylor, Diane
; APPLICANT: Taylor, Diane
; APPLICANT: Governor, Karl F.
; APPLICANT: Governors of the University of Alberta
; APPLICANT: Governors of the University of Alberta
; TILLE OF INVENTION: H. Pylori Pucosyltransferases
; FILE REFERENCE: 019957-019400US
; CURRENT APPLICATION NUMBER: US/10/764,212
; CURRENT PILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                             APPLICANT: Simala-Grant, Joanne
APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Johnson, Karl F.
APPLICANT: Bazila, Daniel James
APPLICANT: Rezila, Daniel James
APPLICANT: Rese Technologies, Inc.
APPLICANT: Governors of the University of Alberta
APPLICANT: Governors of the University of Alberta
FILE REFERENCE: 019957-019400US
FILE REFERENCE: 019957-01940US
CURRENT APPLICATION NUMBER: US/10/764,212
CURRENT PILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 81
SOUTHARE: Patentin Ver. 2.1
SEQ ID NO 66
ILENGTH: 391
                                                                                                                           US-10-764-212-66; Application US/10764212; Sequence 66, Application US-20050164338A1; GENERAL INFORWATION;
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ORGANISM: Helicobacter pylori
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ORGANISM: Helicobacter pylori
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Matches 46; Conservative
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LENGTH: 432
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APPLICANT: The Governers of the University of Alberta, a Canada Corporation APPLICANT: Taylor, Diane E. APPLICANT: Taylor, Diane E. APPLICANT: Taylor, Diane E. Taylor, Diane E. TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND FILE REFERENCE: 07254/049002
CURRENT APPLICATION NUMBER: US/09/733,524
FRIOR APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASESEQ for Windows Version 4.0
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100.0%; Pred. No. 5.9e-30;
tive 0; Mismatches 0;
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OTHER INFORMATION: Strain 11637 from NCTC11637
Sequence 18, Application US/09733524
Patent No. US20020068347A1
GENERAL INFORMATION:
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Matches 41; Conserva
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US-10-449-902-31893
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                                                                               August 11, 2006, 20:11:06; Search time 17.3294 Seconds (without alignments) 1771.230 Million cell updates/sec
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37060,
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06 NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06 NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08 NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-953-349-37062
US-11-056-355B-57749
US-11-056-355B-67719
US-11-056-355B-677110
US-11-056-355B-677110
US-10-953-349-26635
US-11-056-355B-677110
US-10-953-349-26035
US-11-056-355B-67748
US-11-056-355B-67747
US-11-056-355B-67477
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US-11-056-355B-10119
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                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                       239914 segs, 67312017 residues
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                                                          OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
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Perfect score:
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Maximum DB
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                                                                                                                                                             Sequence:
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26 7 1.5 396 7 US-11-056-355B-46490 Sequence 46490, A 27 1.5 396 7 US-11-056-355B-47260 Sequence 47260, A 28 7 1.5 399 7 US-11-056-355B-102107 Sequence 107107, 30 7 1.5 399 7 US-11-056-355B-103107 Sequence 107107, ADD 2 1.5 402 6 US-10-553-436-240 Sequence 107107, ADD 3 1 1.5 402 6 US-10-553-436-240 Sequence 240, ADD 3 1 1.5 436 7 US-11-056-355B-113345 Sequence 240, ADD 3 1 1.5 436 7 US-11-056-355B-113345 Sequence 103106, 34 7 1.5 436 7 US-11-056-355B-113345 Sequence 103106, 36 7 1.5 436 7 US-11-056-355B-113345 Sequence 113345, 36 7 1.5 547 6 US-10-953-349-7497 Sequence 54651, ADD 3 1 1.5 547 6 US-10-949-902-54651 Sequence 5057B, A 40 7 1.5 667 7 US-11-249-902-5057B Sequence 5057B, A 41 7 1.5 607 7 US-11-249-102-250 Sequence 5057B, A 42 7 1.5 607 7 US-11-249-302-5057B Sequence 5057B, A 42 7 1.5 607 7 US-11-349-403-7874 Sequence 7874, A 5 44 7 1.5 607 7 US-11-330-403-14742 Sequence 7874, A 5 6 US-10-449-902-5267B Sequence 5143, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-449-902-5267B Sequence 51474, A 5 6 US-10-4
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## ALIGNMENTS

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US-10-49-902-11893

i Sequence 31893, Application US/10449902

i Sequence 31893, Application US/10449902

i Sequence 31893, Application US/10449902

i REREAL INFORMATION: US20060123505A1

GEREAL INFORMATION: TO Advancement of International Science.

i APPLICANT: Neinonal Institute of Agrobiological Sciences.

APPLICANT: Poundation for Advancement of International Science.

i TITLE OF INVENTION: FULL-INSTITE LANT CDNA AND USES THEREOF

ITTLE REFRENCE: MOA-020511-US

CURRENT PRILICANTON NUMBER: US/10/449,902

CURRENT PRILICATION NUMBER: US/10/449,902

CURRENT PRILICATION NUMBER: US/10/449,902

FRIOR PRILICATION NUMBER: US/10/20-203059

PRIOR PRILICATION NUMBER: US/10/20-303870

PRIOR PRILICATION NUMBER: US/10/20-303870

PRIOR PRILICATION NUMBER: US/10/20-303870

PRIOR PRILICATION NUMBER: US/10/20-303870

PRIOR PRILICATION NUMBER: US/10/20-303870

PRIOR APPLICATION NUMBER: US/10/20-303870

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MATCHES OF SCO. 10/00-10/10/20-20-303870

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US-10-449-902-41833

APPLICANT SINCHARITON SCO. 11833

SEQUENCE 47233, Application US/10449902

MAPPLICANT MALCHORAL INSTITUTE OF MINAMATION: FURL INSTITUTION APPLICANT PROJECT OF Advancement of International Science.

MAPPLICANT PRIBERNEE: MOA-002091-US

SERERALE INFORMATION: FOUNDATION NUMBER: US/10/449, 902

CURRENT APPLICANTON NUMBER: US/10/449, 902

CURRENT APPLICANTON NUMBER: US/10/449, 902

STIER REBERNEE: MOA-002091-US

CURRENT APPLICANTON NUMBER: US/10/449, 902

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CURRENT APPLICANTON NUMBER: US/10/449, 902
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Sequence 26636, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE PATENTION OF 13.3
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
                                                                                                                                                                                                                                              Fragments and Corresponding
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                                                                                                   Sequence 57749, Application US/11056355B; Sequence 57749, Application US/11056355B; Publication No. US20060150283A1; GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav; APPLICANT: Alexandrov, Nickolai; TITLE OF INVENTION: POlypeptides Encoded Thereby; FILE REFERENCE: 2750-1590PUS2; CURRENT APPLICATION NUMBER: US/11/056,355B; CURRENT PILING DATE: 2005-02-14; PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13; NUMBER OF SEQ ID NOS: 119966; SEQ ID NOS: 119966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5%; Score 7; DB 6; Best Local Similarity 100.0%; Pred. No. 47; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.5%; Score 7; DB 7; Best Local Similarity 100.0%; Pred. No. 44; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(245)
; OTHER INFORMATION: Ceres Seq. ID no. 14316381
US-11-056-355B-57749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: prt
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 PLNVALA 201
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    195 PLNVALA 201
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US-11-056-355B-67711
                                                                          RESULT 5
US-11-056-355B-57749
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US-10-953-349-25102
Sequence 25102, Application US/10953349
Sequence 25102, Application US/10953349
Sequence 25102, Application No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
SOFFWARE: Patentin version 3.3
SEQ ID NO 25102
LENGTH: 245
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Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFRENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTING DATE: 2004-09-30
SOFTWARE: PATENTING DATE: 2004-09-30
SOFTWARE: PATENTING DATE: 2004-09-30
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100.0%; Pred. No. 44;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Length 238;
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 47233
LENGTH: 238
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ORGANISM: Zea mays subsp. mays
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Matches 7; Conservative
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US-10-449-902-47233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-25102
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Best Loc Matches

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US-10-953-349-25101
US-10-953-349-25101
Sequence 25101, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION
TOTAL SECURITY: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERRY
TITLE OF INVENTION: ENCONDED THERRY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 25101
LENGTH: 313
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                                                                                                                                    1.5%; Score 7; DB 7;
100.0%; Pred. No. 50;
tive 0; Mismatches
                                               ; NAME/KEY: peptide
; LCCATION: (1)..(276)
; OTHER INFORMATION: Ceres Seq. ID no. 13595882
US-11-056-3558-67710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.5%; Score 7; DB & Best Local Similarity 100.0%; Pred. No. 54; Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                           Sequence 35964, Application US/10449902
Publication No. US20060123505A1
                                                                                                                                  Query Match 1.5
Best Local Similarity 100.
Matches 7; Conservative
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US-10-449-902-35964
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LENGTH: 304
                              FEATURE:
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Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATE: 2004-09-30
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 26635
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Publication No. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brower Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-15500PUS.

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR PELLING DATE: 2006-02-13

PRIOR PELLING DATE: 2004-02-13
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FILE REFERENCE: 2750-1390FUSZ;
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
FRIOR APPLICATION NUMBER: 60/544,190
FRIOR PILING DATE: 2004-02-13
NUMBER OF EGG ID NOS: 119966
SEQ ID NO 67711
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                           Score 7; DB 7;
Pred. No. 47;
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; OTHER INFORMATION: Ceres Seq. ID no. 13595883
US-11-056-355B-67711
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches
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ORGANISM: Triticum aestivum
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SEQ ID NO 67710
LENGTH: 276
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ORGANISM: Triticum aestivum
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Matches 7; Conservative
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-25100
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ORGANISM: Glycine max
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                                                                                                                               Sequence 37061, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: UNDER: 250-1579PUS2

CURRENT APPLICATION UNDER: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PALENTIN VERSION 3.3

SEQ ID NO 37061

LENGTH: 313
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, TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; Sequence 57748, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT PILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
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100.0%; Pred. No. 56;
tive 0; Mismatches
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; LOCATION: (1)..(313)
; OTHER INFORMATION: Ceres Seq. ID no. 14316380
US-11-056-355B-57748
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SEQ ID NO 57748
LENGTH: 313
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Matches 7; Conservative
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Matches 7; Conservative
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263 PLNVALA 269
263 PLNVALA 269
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 57747
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100.0%; Pred. No. 57;
ive 0; Mismatches
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| LOCATION: (1)...(321)

| THER INDEWATION: Ceres Seq. ID no. 14316379

US-11-056-3558-57747
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 25100
LENGTH: 321
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Best Local Similarity 100.
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